

STIC Search Report Biotech-Chem Library

STIC Database Tracking Number: 96572

TO: Gary Nickol

Location: cm-1/8d17/8e12

Art Unit: 1642

Friday, June 20, 2003

Case Serial Number: 513365

From: Mona Smith

Location: Biotech-Chem Library

CM1-6A01

Phone: 308-3278

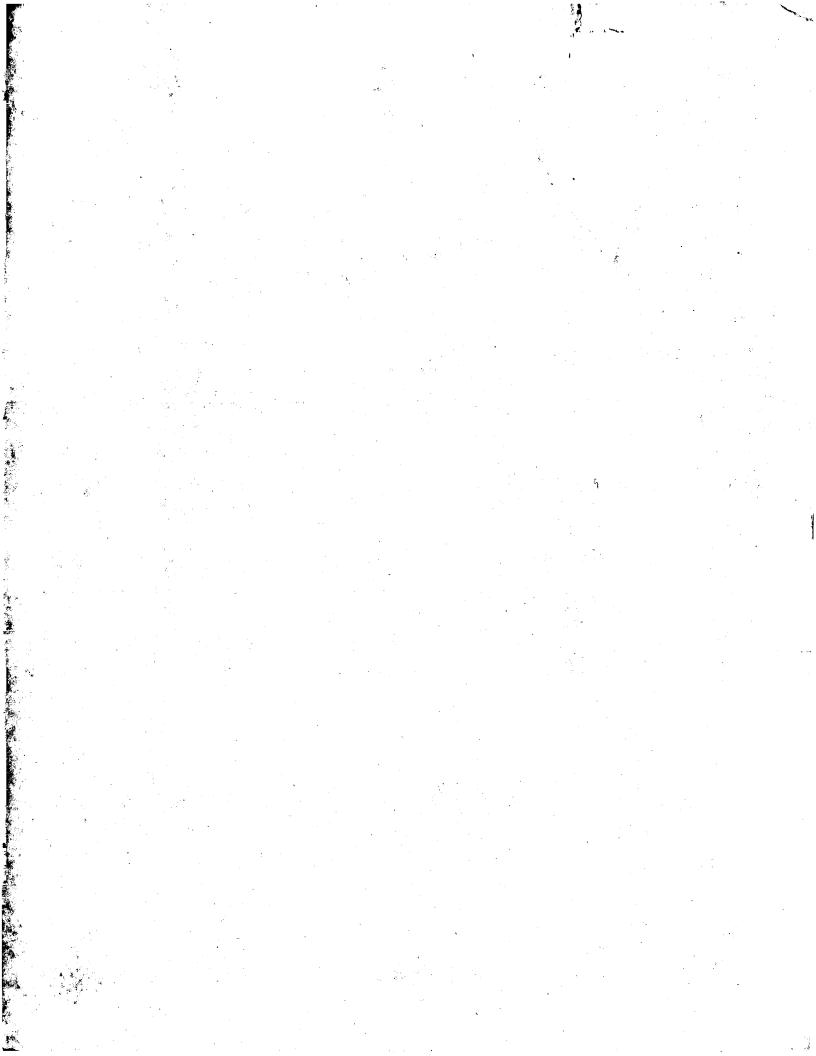
mona.smith@uspto.gov

Search Notes

Thank you for using STIC services
Feel free to contact me if you have any questions.

Mona Smith 308-3278





STIC-Biotech/ChemLib

96592

From: Sent:

Nickol, Gary Friday, June 13, 2003 3:56 PM STIC-Biotech/ChemLib 09/513365

To:

Subject:

Please search the following:

1) DNA of SEQ ID NO:2 2) DNA encoding the amino acids of SEQ ID NO:1

Thanks,

Gary Nickol CM1, AU:1642 Room 8D17, Mailbox 8E12 (703) 305-7143

Searcher: M. Sm.TH
Phone:
Location:
Date Picked Up: 6(16(03
Date Completed: 6120(03
Searcher Prep/Review: 4
Clerical: 5
Online time: 5

TYPE OF SEARCH:
NA Sequences: 2
AA Sequences:
Structures:
Bibliographic:
Litigation:
Full text:
Patent Family:
Othor

VENDOR/COST (where applic	:.)
DIALOG:	==
Questel/Orbit:	_
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Sequence Sys.:	_
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Other (specify):	

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-Q-/cgn2_1/USPTO_spo1/US99513365/runat_16062003_124743_16453/app_query.fasta_1.455
-Q-/cgn2_1/USPTO_spo1/US99513365/runat_16062003_124743_16453/app_query.fasta_1.455
-DB=EST -QFMT=fastap -SUFFIX=rst -MINMATCH=0.1 -LOOPEXT=0
-UNITS-blts -START=1 -END=-1 -MATRIX-blosum62 -TRANS-human40.cd1 -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM-ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER-US09513365_eCGN_1_1_2874_errunat_16062003_124743_16453 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPDEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPDEXT=0.5 -DELOP=6 -DELEXT=7
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DB seq length: 2000000000
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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3175.586 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

RESULT 1 AK012716 AK012716 DEFINITION Mus musculus 10, 11 days embryo whole bod enriched library, clone:2810011M06:simila sequence. ACCESSION VERSION AK012716 VERSION AK012716 GI:12849649 KEYWORDS HTC; CAP trapper. SOURCE Clone:11b:RIKEN full-length enriched mous clone:2810011M06. ORGANISM Mus musculus Eukaryota; Metazoa; Chordata; Craniata; V Mammalia; Eutheria; Rodentia; Sciurognath	ALIGNMENTS	4 681.5 46.0 442 9 ALIIBUB 5 681 46.0 466 9 AIB1872	682 46.0 520 13	690 46.6 555 14 688 46 5 502 12	697 47.1 475 10 692 46.7 477 12	38 700.5 47.3 609 10	724 48.9 561 13 709 47.9 482 9	728 49.2 460 10	741 50.0 574 10 730 49 3 873 14	32 745 50.3 537 9 A	762 51.5 975 14	28 775 52.3 601 14 29 766 51.7 844 12	779.5 52.6 830 12	798 53.9 482 12 780 52.7 692 9	814 33.0 616 9 6	.0 525	20 847 57.2 703 13	852 57.5 566 12 849 57.3 720 9	17 856 57.8 522 13	874 59.0 538 12	13 889 60.0 679 10 14 883 59.6 564 12	12 897 60.6 541 12	920 62.1 675 14	961 64.9 664 14 935 63.1 708 13	1006.5 68.0 798 12	5 1063 71.8 778 13	1094 73.9 793 12	1296 87.5 912 14	1395.5 94.2 1464 11	ilt No. Sco	SOMMANTES
mRNA linear HTC 19-JAN-2002 whole body cDNA, RIKEN full-length HMO6:similar to P331NG2, full insert to P331NG2, full insert claim to P331NG2, full insert claim to P331NG2, full insert to P331NG2, fu		ALII8087 r9225a08 AI818729 wk91d10.x	Br/320/7 Haccourt. B1676689 ic53a06.x	BQ033210 UI-1-CF0-	BE653650 UI-M-AH1- BF513151 UI-H-BW1-	AW342872 fj80b12.y	BJ098630 BJ098630 BA746304 OB56d03 r	AW674790 ba59f06.y	AW674008 ba59f06.x	AI458721 tk13h10.x	BQ934291 AGENCOURT	BQ206861 UI-R-DZ1- BG862842 602797509	BG189892 RST8946 A	BE831862 RC6-MT006	AI186701 qe82d12.x	A1885642 w159h01.x	BI546850 603189754	BE839460 RC3-FN014	B14958/3 G1121G04. B1495874 df121G04.	BF523624 UI-R-C1-1	AV647917 AV647917 BE839427 RC3-FN014	BF114684 7166c08.x	UI-E-	BM719460 UI-E-EJ1- BI460319 603201967	RST29	BI548536 603191255	BE796780 601587557	AG	AK012716 Mus muscu	Description	

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EXPLOTALLOU NOTE: 1-7-22 SUBDIT OF SUBDITION OF SUBDITION
                                                                                                                                                                                      Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Gemomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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Please visit our web site (http://genome.gsc.riken.go.jp/) for
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National Institutes of Health, Mammalian Gene Collection (MGC)

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5', mRNA sequence.
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                   found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
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High quality sequence stop: 587.
Location/Qualifiers
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                                                                                                                       CDNA Library Preparation: Michael Brownstein Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can
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5'-AACCAGCTGCTATCAGCCAGAGTGGCCGTTACGGGCGGG-3' and state of the color of the c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5'-ATTCTAGAGGCCGAGGCGGCCGACATG-dT(30)NN-3'. Full-length enriched library was constructed using the Clontech Creator SMART kit and size-selected to contain the 1-2 kb size fraction (other fractions present in NIH_MGC_126 and NIH_MGC_128). Library created in the laboratory of T. Usdin, M.D., Ph.D. (NIMH, NIH). Note: this is a NIH_MGC_TIBLE.
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/tissue_type="mixed (pool of 40 RNAs)"
/lab_host="DH10B (T1-phage-resistant)"
/note="Vector: pDNR-LIB; Site_1: Sfil (ggccattatggcc);
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                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Scott J. Cain
                                                                                                                                                                                                                                                                                                                                                                                                                                        Creation of genome-wide protein expression libraries using random activation of gene expression Nat. Biotechnol. 19 (5), 440-445 (2001)
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/db_xref="taxon:9606"
/db_xref="taxon:9606"
/clone_lib="athersys RAGE Library"
/cell_line="HT1080"
/note="See 'Creation of Genome-wide Protein Expression / note="See 'Creation of Gene Expression', Nature Biotechnology, in press. Note that even though the cell type indicated is HT1080, since a random activation method was used, these sequence tags are not necessarily expressed in HT1080 under normal circumstances."
a 151 c 216 g 216 t 4 others
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                                           Contact: Robert Strausberg, I
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
                                                                                     National Institutes of Health,
Unpublished (1999)
                                                                                                               NIH-MGC http://mgc.nci.nih.gov/
                                                                                                                                                                          Homo sapiens
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BE796780
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601587557F1 NIH_MGC_7
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            cDNA Library Preparation: Ling Hong/Rubin Laboratory
                                                                                                                                                                                                                                                                                                                                                                                              SerGluSerArgAspLeuCysHisMetAlaAsnGlyIleGluAspCysAspAspGlnPro 177
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Primates;
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 Genomics,
                                                                        Ph.D.
                                                                                                                                               Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                    Mammalian
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 Inc.
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Percent Similarity:
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High quality sequence stop: 769.
Location/Qualifiers
AAAGAAATCCAAGTCAGCAAAGAAAAAGAAACGCTCCAAGGCCAAGCAGGAAAGGGAAAGC
            uLysLysSerLysSerAlaLysLysLysLysArgSerLysAlaLysGlnGluArgGluAl 200
                                                                                                                                                             ArgAspLeu-CysHisMetAlaAsnGlyIleGluAspCysAspAspGlnProProLysGl 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone_lib="NIH_MGC_7"
/tissue_type="small cell carcinoma"
/cell_line="MGC3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3941655"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /lab_host="DH10B (phage-resistant)"
note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2:
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1094.00
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                                                                                                                              University of Iowa
2024 University of Iowa
Tel: 319 356 4866
Fax: 319 356 7171
                                                                                                                                                                             Contact: McCray,
McCray Lab
                                                                                                                                                                                                                                                                                                                                     BM982877.1
                                 Genetics (www.resgen.com).
Seq primer: M13 FORWARD
                                                      Email: paul-mccray@ulowa.edu
Tissue Procurement: Dr. M. J. Welsh, University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University
CDNA Library Arrayed by: Dr. M. Bento Soares, University o
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Res
                                                                                                                                                                                                                             discovery
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US-09-513-365A-1 (1-280) x BM982877
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TAG_LIB-UI-CF-EN1
TAG_TISSUE-Human Lung Epithelial Cell
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/note-"Organ: Lung; Vector: pT7T3-Pac (pharmacia) with a
modified polylinker; Site 1: EcoR I; Site 2: Not I;
UI-CF-ENI is a normalized cDNA library containing the
following tissue(s): Primary Lung Cystic Fibrosis
Epithelial Cells. The library was constructed according to
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
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/db_xref="taxon:9666"
/clone="UI-CF-ENI-acs-d-05-0-UI"
/clone_1ib="UI-CF-ENI"
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Allgnment Scores: Pred. No.: 1006.50 Matches: 209 Percent Similarity: 95.438 Best Local Similarity: 95.438 Ouery Match: 12 Ouery Match: 12 Oy 62 GluIleAspAspValTyrGluLysTyrLysLysGluAspAspLeuAsnGlnLysLysArg Gaps: Oy 63 GAAATTGATAT-GTCTACGCAAAATATAG-AAAGAAGATGAATGAAAAAAA- CTACAGCAGCTTCTCCAGAGAGCACCTATTAT-AGTCAAGAAGATGAAAAAA- Oy 82 LeuGlnGlnLeuLeuGlnArgAlaLeuIleAsnSerGlnGluLeuGlyAspGluLysIle Oy 83 LeuGlnGlnLeuLeuGlnArgAlaLeuIleAsnSerGlnGluLeuGlyAspGluLysIle Oy 84 LeuGlnGlnLeuLeuGlnArgAlaLeuIleAsnSerGlnGluLeuGlyAspGluLysIle Oy 85 LeuGlnGlnLeuLeuGlnArgAlaLeuIleAsnSerGlnGluLeuGlyAspGluLysIle Oy 86 CTACAGCAGCTTCTCCAGAGAGCACCTATTAT-AGTCAAGAATGGGGAAGAAAAA- Oy 10 GlnlleValThrGlnMetLeuGluLeuValGluAsnArgAlaArgGlnMetGluLeuHis Oy 10 GlnlleValThrGlnMetLeuGluLeuValGluAsnArgAlaArgGdnMetGluLeuHis Oy 10 GlnlleValThrGlnArgAlaCuCaGAATTGGGGAAGACAAATGGAGTTACAC Oy 11	216 431 9900 216 361 9596 1: scain@athersys.com quality sequence stop: 531.	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 798) AUTHORS Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R., Cain,S., Leventhal,C., Thornton,M., Ramachandran,R., Whitington,J., Lerner,L., Costanzo,D., McElligott,K., Boozer,S., Mays,R., Smith, E., Veloso,N., Kilka,A., Hess,J., Cothren,K., Lo,K., Offenbacher J., Danzig,J. and Ducar,M. TITLE Creation of genome-wide protein expression libraries using random activation of gene expression JOURNAL Nat. Biotechnol. 19 (5), 440-445 (2001) MEDLINE CONTECT: Scott J. Cain Athersys, Inc. 3201 Carnegie Ave., Cleveland, OH 44115, USA	SULT 7 184055/c BG184056 CUS BG184056 CESSION BG184056 RST2972 Athersys RAGE Library Homo sapie RSION BG184056 SG184056.1 GI:13705743 YWORDS EST URCE human. ORGANISM Homo sapiens Eukaryota; Metazoa; Chordata; Craniata;	Db 255 GGGAAATGGTATTGCCCAAAGTGCAGGGGAGATAATGAGAAAACAATGGACAAAAGTACT 196 Oy 271 GlulysThrlysLysAspArgArgSerArg 280
COMMENT Contact: Soares, MB Program for Rat Gene Discovery and Mapping University of Iowa 451 Eckstein Medical Research Building Iowa City, IA 52242, USA Tel: 319 335 8250 Fax: 319 335 9365 Email: msoares@blue.weeg.ulowa.edu Tissue Procurement: Dr. Gregg Hageman cDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa CDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa Clone Distribution: Researchers may obtain clones from Research Genetics (www.resgen.com). Seq primer: M13 Reverse. I664 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="UI-E-EJI-ajf-g-22-0-UI" /clone="UI-E-EJI-ajf-g-22-0-UI" /tissue_type="fetal eyes, lens, eye anterior segment,	8 0 0 0 ION UI-E-EJ1-ajf-g-2: UI-E-EJ1-ajf-g-2: ON BM719460.1 GI:1: S EST. human. ISM Homo sapiens Eukaryota; Metazo Mammalia; Euther: CE 1 (bases 1 to 66 RS Bonaldo, M.F., Len discovery AL Genome Res. 6 (9) NE 97044477	Db 384 CCTGTTGGCATTGCAATAGATCCTACATACTGCTTATGCAACCAAGTGTCT 325 Qy 222 TyrGlyGluMetileGlyCysAspAsnGluGlnCysProIleGluTrpPheHisPheSer 241	162 AspLeuCysHisMetAlaAsnGlyIleGluAspCysAspAspGlnProProLysGluLys	Db 624 TCACAGTGTTTCCAAGATCCTGCTGAAAGTGAACGAGCCTCAGATAAAGCAAAGATGGAT 565 Oy 142 SerSerGlnProGluArgSerSerArgArgProArgArgGlnArgThrSerGluSerArg 161

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US-09-513-365A-1 (1-280) x BM719460
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     BI460319
BI460319.1
                                                     mRNA sequence.
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modified polylinker; Site_1: EcoR I; Site_2: Not I;
UI-B-EJ1 is a subtracted cDNA library constructed
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Email: cgapbs remail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.

CDNA Library Preparation: Michael J. Brownstein (NHGRI)
CDNA Library Preparation: Michael J. Brownstein (NHGRI)
CDNA Library Arrayed by: The I.M.A.G. E. Consortium (LLN
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information
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1 (bases 1 to 708)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)
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                                                                                                                          ArgLeuGlnGlnLeuLeuGlnArgAlaLeuIleAsnSerGlnGluLeuGlyAspGluLys
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                                                                                                   CGTCTACAGCAGCTTCTCCAGAGAGCACTAATTAATAGTCAAGAATTGGGAGATGAAAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note-*Organ: testis; Vector: pBluescriptR (modified pBluescript KS+); Site1: BamH; Site2: Sall-XhoI (gtcg:); Oligo-dT primed using primer 5:-TTTTTTTTTTTTTVN-3; size-selected for average insert size 2.2 kb and normalized to ROT 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIMH/NHGRI, National Institutes of Health). Note: this is a NIM_MGC Library.*

a 163 c 213 g 122 t 1 others
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/lab_host="DH10B"
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/clone="IMAGE:5267729"
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Sali-Xhoi (gtcgag

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Query Match: DB:

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BASE COUNT

Alignment Scores:

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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tissue Procurement: Dr. Gregg Hageman
CDNA Library preparation: Dr. M. Bento Soares, Univeristy
CDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy
DNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iov
Clone Distribution: Researchers may obtain clones from Re
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Program for Rat Gene Discovery and Mapping University of Iowa
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Genetics (www.resgen.com).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eckstein Medical Research Building Towa City, 319 335 8250 319 335 9565
     /dev_stage="fetal and adult"
//lab_host="DH10B (Life Technologies) (T1 phage resistant)"
//lab_host="DH10B (Life Technologies) (T1 phage resistant)"
//lab_host="DT9an: eye; Vector: pT7T3-Pac (Pharmacia) with a
modified polylinker; Site_1: ECOR I; Site_2: Not I;
UI-E-EJ1 is a subtracted cDNA library constructed
according to Bonaldo, Lennon and Soares, Genome Research,
6:791-806, 1996. First strand cDNA synthesis was primed
with an oligo-dT primer containing a Not I site. Double
stranded cDNA was ligated to an ECOR I adaptor, digested
with Not I, and cloned directionally into pT7T3-Pac
vector. The oligonucleotide used to prime the synthesis of
first-strand cDNA contains a library tag sequence that is
located between the Not I site and the (dT).B tail. The
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Soares,
                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
/clone="UI-E-EJI-ajf-g-22-0-UI"
/clone_lib="UI-E-EJI"
/tissue_type="fetal eyes, lens, eye anterior segment,
optic nerve, retina, Retina Foveal and Macular, RPE and
                                                                                                                                                                                                                                                  Choroid"
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Eutheria; Primates; Catarrhini; Hominidae
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US-09-513-365A-1 (1-280) x BM682789
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EST.
                                                                                                                       mRNA sequence
BI091047
NIH-MGC http://mgc.nci.nih.gov/.
                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae 1 (bases 1 to 891)
                                                                    Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     optic nerve, CCATTAAGTG; retina, CCGCG; Retina Foveal ar Macular, GTCC; RPE and Chorold, ACCTA. This library was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute (NEI).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                    ArgArgProArgArgGlnArgThrSerGluSerArgAspLeuCysHismetAlaAsnGly 169
AsnGluGlnCysProIleGluTrpPheHisPheSerCysValSerLeuThrTyrLysPro
                                               AsnGluProThrTyrCysLeuCysAsnGlnValSerTyrGlyGluMetIleGlyCysAsp
                                                                                             AAACGCTCCAAGGCCAAGCAGGAAAGGGAAGCTTCACCTGTTGAGTTTGCAATAGATCCT
                                                                                                           LysArgSerLysAlaLysGlnGluArgGluAlaSerProValGluPheAlaIleAspPro 209
                                                                                                                                                                           GGTGGTTAATCGGCA-AGACATATGGAGTTACACTCACAGTGTTTCCAAGATCCTGTCTG
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                                                                                                                                                           luSerGluArgAlaSerAspLysAlaLysMet-AspSerSerGlnProGluArgSerSer 149
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199 c 149 g 306 t
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/clone_lib="NIH_MGC_10"
/cell_line="MGC36"
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/db_xref="taxon:9606"
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AUTHORS
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                                                                US-09-513-365A-1 (1-280) x BF114684 (1-541)
                                                                                                                                   Query Match:
                                                                                                                                                          Percent Similarity:
Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

This clone is available royalty-free through LLNL; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

Seg primer: -400P from Gibco
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BF114684
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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MetLeuGlyGlnGlnGlnGlnGlnLeuTyrSerSerAlaAlaLeuLeuThrGlyGluArg
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                            /note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from five normalized libraries were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 5 libraries. The pools consisted of the following libraries and cloneIDs: Soares NbHFP pool 1: 309384-330919, 333208-325895 Soares NbHFP pool 1: 150407, 151176-152327 Soares NbHFB-9W pool 1: 758280-760583, 772104-774407 Soares NbHFR-pool 1: 758280-760583, 772104-774407 Soares NbHFR-pool 1: 758280-760583, 320136-322823, 326280-32663 Soares NbHOT pool 1: 723720-726407, 739080-740999 Subtraction by Bento Soares and M. Fatima Bonaldo."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone="IMAGE:3391406"
/clone_lib="Soares_NSF_F8_9W_OT_PA_P_S1"
/lab_host="DH10B"
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/db_xref="taxon:9606"
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COMMENT COMMENT FEATURES SOULC	AUTHORS TITLE JOURNAL	RESULT 13 AV647917 LOCUS DEFINITION ACCESSION VERSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE		Qy 1 Db 3 Db 1	0y 0y 1 0y 1 0y 1 0y 1	O D D D D D D D D D D D D D D D D D D D
Contact: Zeguang Han Chinese National Human Genome Center at Shanghai 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai 201203, P. R. China Tel: 86-21-50801919(ex.45) Fax: 86-21-50801919(ex.45) Email: hanzg@chgc.sh.cn This clone is available at CHGC in Shanghai. Location/Qualifiers 1. c.679 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="GLGEDD03" /clone="ib-"GLC" /tissue_type="corresponding non cancerous liver tissue" /dev_stage="Adult" /lab_host="SOLR" /lab_host="SOLR" /note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:	Xu,X., Huang,J., Xu,Z., Qian,B., Zhu,Z., Yan,Q., Cai,T., Zhang,X., Xiao,H., Qu,J., Liu,F., Huang,Q., Cheng,Z., Li,N., Du,J., Hu,W., Shen,K., Lu,G., Fu,G., Zhong,M., Xu,S., Gu,W., Huang,W., Zhao,X., Hu,G., Gu,J., Chen,Z. and Han,Z. Insight into hepatocellular carcinogenesis at transcriptome level by comparing gene expression profiles of hepatocellular carcinoma with those of corresponding noncancerous liver proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)	AV647917 AV647917 GLC Homo sapiens cDNA clone GLCBDD03 3', mRNA sequence. AV647917 AV647917.1 GI:9868931 EST. human. Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 679)	141 AspSerSerGlnProGluArgSerSerArgArgProArgArgGlnArgThrSerGluSer 160	101 IleGlnIleValThrGlnMetLeuGluLeuValGluAsnArgAlaArgGlnMetGluLeu 120	41 ASPMETGINATGASNVALSERVALLEUARTGGIULEUARTSANTLYSTYTGINGIUTHTLEU 60	ATGTTAGGGCAGCAGCAGCAGCAGCTGTACTCGTCGCTGCCATCCTGACCGGGGAGCGG SerArgLeuLeuThrCysTyrValGlnAspTyrLeuGluCysValGluSerLeuProHis
RESULT 14 BEB39427/c BEB39427/c BEB39427/ LOCUS	Qy 161 ArgAspLeuCysHisMetAlaAsnGlyIleGluAspCysAspAspGlnProProLysGlu 180	Oy 101 IleGlnIleValThrGlnMetLeuGluLeuValGluAsnArgAlaArgGlnMetGluLeu 120	Qy 61 LysGluIleAspAspValTyrGluLysTyrLysLysGluAspAspLeuAsnGlnLysLys 80	Qy 21 SerArgLeuLeuThrCysTyrValGlnAspTyrLeuGluCysValGluSerLeuProHis 40	### 189.00 Matches: 17	" 151 c 206 g. 116 t .55e-66 Length:

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=RC3-FN0143-190
700-022-d12xt3=2000-07-19xt4=1)
Seq primer: puc 18 forward
High quality sequence start: 18
High quality sequence stop: 564.
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Ludwig Institute for Cancer Research
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AspSerSerGlnProGluArgSerSerArgArgProArgArgGlnArgThrSerGluSer 16(
                                                     HisSerGlnCysPheGlnAspProAlaGluSerGluArgAlaSerAspLysAlaLysMet 140
                                                                                                       CGTCTACAGCAGCTTCTCCAGAGAGCACTAATTAATAGTCAAGAATTGGGAGATGAAAAA
                                                                                                                                                                                                 ArgLeuGlnGlnLeuLeuGlnArgAlaLeuIleAsnSerGlnGluLeuGlyAspGluLys 100
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/db_xref="taxon:9606"
/clone_lib="FN0143"
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RESULT 15
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UI-R-C1-lc-d-10-0-UI 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LLNL (info@image.llnl.gov). IMAGE ID-
Seq primer: M13 Forward.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: msoares@blue.weeg.uiowa.edu
CDNA Library Preparation: M.B. Soares Lab Clone distribution:
CDNA Library Preparation: through Research Genetics (www.resge
This clone is also available through the I.M.A.G.E. Consortiu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      University of Iowa
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Program for Rat Gene Discovery and Mapping
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rattus norvegicus
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/lab_host="DHIOB (Life Technologies)"
/note="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-C1
library is a subtracted library derived from the UI-R-C0
library, which is a subtracted library derived from the
UI-R-A1 and UI-R-E1 libraries. The UI-R-A1 library
consisted of a mixture of individually tagged normalized
libraries constructed from rat placenta, adult lung,
brain, liver, kidney, heart, spleen, ovary, and muscle.
The UI-R-E1 library consisted of a mixture of
individually tagged normalized libraries constructed from
8, 12 and 18-day embryo. The tag is a string of 3-5
nucleotides present between the Not I site and the
oligo-dT track which allows identification of the library
of origin of a clone within the mixture. The subtracted
library (UI-R-C1) was constructed as follows: PCR
amplified cDNA inserts from UI-R-C0 clones from which 3'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Res. 6 (9),
                                                                                       ESTs had been derived was used as a driver in a hybridization with the UI-R-CO library in the form of single-stranded circles. The remaining single-stranded circles (subtracted library) was purified by hydroxyapatite column chromatography, converted to
               double-stranded circles and electroporated into DH10B bacteria (Life Technologies) to generate the UI-R-C1 library. This procedure has been previously described
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone="UI-R-C1-lc-d-10-0-UI"
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/db_xref="taxon:10116"
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and Soares,
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Consortium at
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Search completed: June Job time : 1433 secs	Оу 1	Qy 1:	Оу 1: Db 1:	Qy 1: Db 2:	Qy	Qy Db 3:	Qy Db 4:	Qy Db 4	Qy Db 5	Alignment Scores: Pred. No.: Score: Score: Percent Similarity: Best Local Similarity: Query Match: DB: US-09-513-365A-1 (1-28	BASE COUNT ORIGIN
20,	177 ProProLysGluLys	157 ThrSerGluSerArg		117 GlnMetGluLeuHis: 	97 GlyAspGluLysIle	77 AsnGlnLysLysArg	57 GlnGluThrLeuLys	37 SerLéuProHisAspl 	17 ThrGlyGluArgSer	5.3 874 98. 96. 59. 12	95 a 135 .
2003, 03:50:01	ProProLysGluLysLysSerLysSerAlaLysLysLysLysArg 	ThrSerGluSerArgAspLeuCysHisMetAlaAsnGlyIleGluAspCysAspAspGln	LysAlaLysMetAspSerSerGlnProGluArgSerSerArgArgProArgArgGlnArg :::	GlnMetGluLeuHisSerGlnCysPheGlnAspProAlaGluSerGluArgAlaSerAsp 	GlyAspGluLysIleGlnIleValThrGlnMetLeuGluLeuValGluAsnArgAlaArg 	AsnGlnLysLysArgLeuGlnGlnLeuLeuGlnArgAlaLeuIleAsnSerGlnGluLeu 	GlnGluThrLeuLysGluIleAspAspValTyrGluLysTyrLysLysGluAspAspLeu 	SerLéuProHisAspMetGlnArgAsnValSerValLeuArgGluLeuAspAsnLysTyr 	ThrGlyGluArgSerArgLeuLeuThrCysTyrValGlnAspTyrLeuGluCysValGlu 	### 188e-65 Length:	c 117 g 191 t
	sLysArg 191 ::: AAAAAAA 12	yIleGluAspCysAspAspGlr ::: GATTGATGACTGCGATGATCAC	rArgArgProArgArgGlnArg CAGAAGACCTCGAAGACAGCGG	aGluSerGluArgAlaSerAsp TGAAAGTGAGCGGGCCTCAGA	uLeuValGluAsnArgAlaArç 	aLeuIleAsnSerGlnGluLe TTAATCAATAGCCAAGAATTO	STyrLysLysGluAspAspLe TATAAGAAAGAAGATGATTC!	uArgGluLeuAspAsnLysTy1 CGGGAGCTGGACAACAATAC	nAspTyrLeuGluCysValGlu 	538 169 3 3	
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-MODEL-frame+_D2n.model -DEV-xlp
-C-/cgn2_1/USPTO_spool/US09513365/runat_16062003_124742_16434/app_guery.fasta_1.455
-DB-N_Geneseq_101002 -QFMT-fastap -SUFFIX=rng -MINMATCH-0.1 -LOOPCL-0
-LOOPEXT-0 -UNITS-blts -START-1 -END-1 -MATRIX-blosum62 -TRANS-human40.cdi
-LIST-45 -DOCALIGN-200 -THR_SCORE-pct -THR_MAX-100 -THR_MIN-0 -ALIGN-15
-MODE-LOCAL -OUTFMT-pto -NORM-ext -HEAPSIZE=500 -MINLEN-0 -MAXLEN-200000000
-USER-US09513365_GCGN_1 1_396_erunat_16062003_124742_16434 -NCPU-6 -ICPU-3
-USER-US09513365_GCGN_1 1_396_erunat_16062003_124742_16434 -NCPU-6 -ICPU-3
-NO_MMAP -LARGEQUERY -NEG_SCORES-0 -WAIT -DSPBLOCK-100 -LONGLOG
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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LysLysSerLysSerAlaLysLysLysLysArgSerLysAlaLysGlnGluArgGluAla
                                                                                                                                               ArgAspLeuCysH1sMetAlaAsnGlyIleGluAspCysAspAspGlnProProLysGlu
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                                                                                        AAGAAATCCAAGTCAGCAAAGAAAAAGAAACGCTCCAAGGCCAAGCAGGAAAGGGAAGCT
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                                    US-09-513-365A-1 (1-280)
                                                                                             Score:
                                                                                                                                               The present sequence is a DNA encoding tumour suppressor homologue protein, p331NG2 which is homologous to human tumour suppressor proparation. The tumour suppressors of the invention are involved in the regulation of cell proliferation and in the control of cellular aginanchorage dependence and apoptosis. The tumour suppressor protein, p471NG3, nucleic acids encoding it and antibodies against it are us for diagnosis, prevention and treatment of tumours and cancers. The p471NG3 DNA is also used in gene therapy.
                                                                                                                                Sequence 1080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tumour suppressor; p4 anchorage dependence;
                                                                                                                                                                                                                                    Disclosure;
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              Location/Qualifiers
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                                                                                                                                       protein; TUSUP; human; cancer; treat;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TUSUP sequence encodes the human tumour suppressor (TUSUP) protein. The TUSUP sequence was identified from a human lung cDNA library. The protein is 240 amino acids in length and has one potential cAMP and cGMP dependent protein kinase phosphorylation site, nine potential protein kinase c phosphorylation sites, five potential casein kinase phosphorylation sites, and one potential tyrosine kinase phosphorylation sites, and chemical similarity to p33. TUSUP can be used to treat or prevent cancer, particularly of the reproductive or gastrointestinal tracts or of the immune system. Agonists of the TUSUP protein can be used to raise TUSUP specific binding agents and potential therapeutic agents. The TUSUP nucleotide sequence can be used in gene therapy and as a source of diagnostic probes and primers.
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P-PSDB;
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                                                              CCGTCGCGGATCCTGGCTCCGCAAACGTTAAAGGAAATTGATGATGTCTACGAAAAATAT
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GluThrLeuLysGluIleAspAspValTyrGluLysTyrLysLysGluAspAspLeuAsn CTGCCTTTCGACCTGCAGAGGAACGTCTCGCTGATGCGGGAGATCGACGCCAAATACCAA

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LeuProHisAspMetGlnArgAsnValSerValLeuArgGluLeuAspAsnLysTyrGln

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US-09-513-365A-1 (1-280) x AAA53790

(1-2817)

Best Local Similarity: Query Match:

Percent Similarity:

7.04e-74 874.50 77.41% 61.11% 59.05%

Mismatches: Indels: Matches: Conservative:

2817 165 44 50

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gene, each having their own promoter (la) produces a protein identical to INOI Expression of one promoter (la) produces a protein identical to INOI Expression of a second promoter (lb) produces a protein having an identical C-terminal fragment to INOI but an additional 104

CC N-terminal amino acids. The newly discovered protein has been designated p37ING1 (Wild type: p33ING1), p37ING1 has the characteristics of an oncogene. When overexpressed in cells (even those expressing wild type p53) p37ING1 is able to cause proliferation or transformation of those cells. Thus detecting a nucleic acid encoding exon 1b of ing1 by hybridisation with an included nucleic acid having the sequence of exon 1b of ing1 or its antisense sequence can identify individuals expressing the concegenic form of ing1. Novel peptide sequences taken from the 104 N-terminal peptide of p37ING1 can also be used to raise antibodies that can also be used in detection methods for the p37ING1 variant.

CC The polypeptides may be useful in gene therapy for treatment of cell produces and identify cancers and for diagnosing and concegning the sequences of expressing the sequence of expressions the sequence of expressions the sequen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   remains unknown but p53 has been found to act in cooperation with ING1. Functional cooperation between ING1 and p53 suggested that ING1 encoded a tumour suppressor protein that functioned within the p53 pathway. This data suggested a possible role for ING1 in head and neck cancers and chromosomal location of the ING1 placed it within a region that is frequently rearranged in head and neck cancers. Large scale analysis of tumours involving ING1 has not revealed mutations in ING1 nor significant variations in its expression suggesting that ING1 was not a useful gene to study in cancer etiology. However, alternative initiation exons of the ing1
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Sequence 2817
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Expression of one promoter (la) produces a protein identical to ING1. Expression of a second promoter (lb) produces a protein having an identical C-terminal fragment to ING1 but an additional 104 N-terminal amino acids. The newly discovered protein has been designated p37ING1 (Wild type: p33ING1). p37ING1 has the characteristics of an oncogene. When overexpressed in cells (even those expressing wild type p53) p37ING1 is able to cause proliferation or transformation of those cells. Thus detecting a nucleic acid encoding exon 1b of ingl by hybridisation with an isolated nucleic acid having the sequence of exon 1b of ingl cor its antisense sequence can identify individuals expressing the oncogenic form of ingl. Novel peptide sequences taken from the 104 N-terminal peptide of p37ING1 can also be used to raise antibodies that can also be used in detection methods for the p37ING1 can also be used to raise antibodies that can also be used to useful in gene therapy for treatment of cell proliferation disorders, especially cancers and for diagnosing and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 p53 pathway. This data suggested a possible role for ING1 in head and neck cancers and chromosomal location of the ING1 placed it within a region that is frequently rearranged in head and neck cancers. Large scale analysis of tumours involving ING1 has not revealed mutations in ING1 nor significant variations in its expression suggesting that ING1 was not a useful gene to study in cancer etiology. However, alternative initiation exons of the ing1 gene, each having their own promoter have been discovered.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the p53 pathway occurs in a much larger proportion of tumours. In many cases the mechanism of functional inactivation of the p53 gene remains unknown but p53 has been found to act in cooperation with ING1. Functional cooperation between ING1 and p53 suggested that ING1 encoded a tumour suppressor protein that functioned within the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence encodes a human cancer associated antigen. The sequence is a variant of the ING1 gene, which is a tumour The sequence is a variant of the ING1 gene, which is a tumour suppressor gene candidate. The cancer associated antigen polynucleotides and polypeptides are useful for screening for the possible presence of a pathological condition in a subject such as cancer. The cancer associated antigen polypeptides are useful for producing vaccines.
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                                                                                     AspProAsnGluProThrTyrCysLeuCysAsnGlnValSerTyrGlyGluMetIleGly
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                                                                                                                                       1065
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227

247

147 825 136 765 117 705 97 645 77 585 57 525 37

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cc combination, to specifically recognise epitopes of ING1 (inhibitor of CC growth 1) protein isoforms. ING1 is a tumour suppressor gene and its CC expression is regulated through the cell cycle, peaking in the S phase. CC Expression of ING1 is down regulated in breast tumours and lymphoid CC malignancies. Overexpression of a construct containing the ING1 gene is CC able to inhibit cell growth by reducing the fraction of cells which enter CC into the S phase. The monoclonal antibodies are useful for detecting an CC ING1 protein in a cell, which involves selecting a cell that ectopically or endogenously expresses ING1 protein. The anti-ING1 monoclonal antibody combination consists of two or more antibodies of CAb1-CAb10 (not two different isoforms of ING1. The antibodies are also useful for diagnosing a disease e.g. tumour or medical condition in an animal CC (preferably, human) associated with aberrant levels of an ING1 protein.
             RESULT 8
ABK86977
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26-FEB-1999;
15-NOV-1996;
08-DEC-1995;
22-MAR-2000;
                                                                                                                                                                                                                                  Novel monoclonal antibody which specifically recognizes epitope ING1, inhibitor of growth 1 protein, and designated CAb1-10, use detecting two different isoforms of ING1 and diagnosing a medical
                                                                                                                                                                                                                                                                                                 WPI;
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                                                                                                                                                                                                   Disclosure;
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DB; AAU79587.
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                                                                                                                                                                                                                                                                                                                                                BOLAND
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99US-0258372.
96US-0751230.
95US-0569721.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ss; monoclonal antibody;
suppressor; cell cycle; l
anti-ING1; CAb; isoform;
                                                                                                                                                                                                                                                                                                                                                                                  2000US-0532868
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                                                                                                                                                                                                 15pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "p33ING1b"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (ING1) isoform, p33ING1b,
                                                                                                                                                                                                   English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; epitope; inhibitor of growth 1;
breast tumour; lymphoid malignancy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  diagnosis;
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Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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Pred. No.:
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AAAGCCCTGGAGAAATCCAAAAAAGAGAGG
                                 AspProAsnGluProThrTyrCysLeuCysAsnGlnValSerTyrGlyGluMetIleGly
                                                                                                                                                     LysLysLysArgSerLysAlaLysGlnGluArgGluAlaSerProValGluPheAlaIle
                                                                                                                                                                                        AsnGlyIleGluAspCysAspAspGlnProProLysGluLysLysSerLysSerAlaLys
                                                                                                                                                                                                                            GlnLysLysArgLeuGlnGlnLeuLeuGlnArgAlaLeuIleAsnSerGlnGluLeuGly
                                                                                                                                                                                                                                                                                                                                                                                                GluThrLeuLysGluIleAspAspValTyrGluLysTyrLysLysGluAspAspLeuAsn
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          LysSerThrGluLysThrLysLysAspArg
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                                                                                                                                            AAGAAGAAGCGCTCCAAGGCCAAGGCGGAGCGAGAGGCGTCCCCTGCCGACCTCCCCATC
                                                                                                                                                                                CACGACCACGACGACGGCGCCTCGGGCACACCCAAGGAGAAGAAGGCCAAGACCTCCAAG
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59.26%
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Conservative:
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RESULT

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Alignment Scores:
                    Pred. No.:
                                                                                                         CC ING1 encoded a tumour suppressor protein that functional cooperation between ING1 and p53 suggested that CC ING1 encoded a tumour suppressor protein that functioned within the CC p53 pathway. This data suggested a possible role for ING1 in head CC and neck cancers and chromosomal location of the ING1 placed it CC within a region that is frequently rearranged in head and neck cancers. Large scale analysis of tumours involving ING1 has not revealed mutations in ING1 nor significant variations in its CC cancer ethology. However, alternative initiation exons of the ing1 CC cancer ethology. However, alternative initiation exons of the ing1 CC cancer ethology. However, alternative initiation exons of the ing1 CC cancer ethology. However, alternative initiation exons of the ing1 CC cancer ethology. However, alternative initiation exons of the ing1 CC cancer ethology. However, alternative initiation exons of the ing1 CC cancer ethology. However, alternative initiation exons of the ing1 CC cancer ethology. However, alternative initiation exons of the ing1 CC cancer ethology. However, alternative initiation exons of the ing1 CC cancer ethology. However, alternative initiation exons of the ing1 produces a protein identical to CC cancer ethology. However, alternative find by produces a protein having CC cancer ethology. However, alternative find having the sequence can identify individuals expressing the CC content of the cancer can also be useful in gene therapy for treatment of cell CC proliferation disorders, especially cancers and for diagnosing and CC studying cancers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Detecting nucleic acid encoding exon 1b of ing1, useful for diagnosing and treating cancer, comprises contacting sample with isolated nucleic acid comprising sequence of exon 1b and detecting hybridized products
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      p53; tumour; cancer; detection; antibody; hybridisation; exon 1b; ING1; ing1; p33ING1; p37ING1; oncogene; gene therapy; diagnosis; proliferation disorder; transformation; transformed cell; mouse;
                                                                 Sequence 1835 BP; 541 A; 387 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the p53 pathway occurs in a much larger proportion of tumours. In many cases the mechanism of functional inactivation of the p53 gene remains unknown but p53 has been found to act in cooperation with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 17; Fig 6; 134pp; English
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100 LysIleGlnIleValThrGlnMetLeuGluLeuValGluAsnArgAlaArgGlnMetGlu 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         80 LysargLeuGlnGlnLeuLeuGlnArgAlaLeuIleAsnSerGlnGluLeuGlyAspGlu :::||||:::
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60 LeuLysGluIleAspAspValTyrGluLysTyrLysLysGluAspAspLeuAsnGlnLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       66 CGCCGGGTACTGCACTGCATCCAGAGGGCCCTGATCCGCAGCCAGGAGCTAGGCGATGAG
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                                                                                                                                                                                                                                                                                                                    CTGGAGAAGTCCAAGAAAGAGAGAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LeuHisSerGlnCysPhe-----GlnAspProAlaGluSerGluArgAlaSerAsp
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                                                                                                                                                                                                                                                                                                                                                   ThrGluLysThrLysLysAspArg 277
                                                                                                                                                                                                                                                                                                                                                                                     AAGGGCAAGTGGTACTGCCCCAAGTGCCGTGGGGAGAGCGAGAAGACCATGGACAAAGCC
                                                                                                                                                                                                                                                                                                                                                                                                     AACGACGAATGCCCCATCGAGTGGTTCCACTTCTCCTGCGTGGGGCTCAACCATAAACCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AsnGluGlnCysProIleGluTrpPheHisPheSerCysValSerLeuThrTyrLysPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AACGAGCCCACGTACTGTCTGTGCAACCAGGTCTCCTACGGGGAGATGATCGGCTGTGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AsnGluProThrTyrCysLeuCysAsnGlnValSerTyrGlyGluMetIleGlyCysAsp
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                                                                                                                                                 sequence of a human cancer associated
                                                                                                                                                                                  (first
                                Location/Qualifiers 16..900
/transl_except= "(pos: 25..30,
                                                                                                                  antigen; ING1; tumour
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        76.75%
61.40%
50.30%
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Indels:
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                                                                                                                  suppressor; cancer; vaccine;
 aa: Cys)'
                                                                                                                                                 antigen
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Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                                                                              Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence encodes a human cancer assuctance.

The sequence is the wildtype of the ING1 gene, which is a tumour the sequence is the wildtype of the ING1 gene, which is a tumour suppressor gene candidate. The cancer associated antigen polynucleotides suppressor gene useful for screening for the possible presence of and polypeptides are useful for screening for the possible presence of anathological condition in a subject such as cancer. The cancer anathological condition in a subject such as cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Isolated cancer associated nucleic acid molecule identified by SEREX (serological identification of antigens by recombinant expression cloning) technique, useful in nucleic acid based therapies to treat cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI;
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                                                                                                                                                                                                                                                                                                                                                                                                       No.:
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24-OCT-2000;
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)B; AAB84697.
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LeuGlyAspGluLysIleGlnIleValThrGlnMetLeuGluLeuValGluAsnArgAla 115
                                                                                                                                                                                                                                                                       TyrGlnGluThrLeuLysGluIleAspAspValTyrGluLysTyrLysLysGluAspAsp
                                                         {\tt GlnProGluArgSerSerArgArgProArgArgGlnArgThrSerGluSerArgAspLeu}
                                                                                 GGCAACAGCGGCAAGGTTGGCGCGGACAGGCCCAATGGCGATGCGGTAGCGCAGTCTGAC
                                                                                                                                                   ArgGlnMetGluLeuHisSerGlnCysPheGlnAspProAlaGlu---
                                                                                                                                                                           CTGGGCGACGAGAAGATCCAGATCGTGAGCCAGATGGTGGAGCTGGTGGAGAACCGCACG
                                                                                                                                                                                                                          LeuAsnGlnLysLysArgLeuGlnGlnLeuLeuGlnArgAlaLeuIleAsnSerGlnGlu
                                                                                                                              CGGCAGGTGGACAGCCACGTGGAGCTGTTCGAGGCGAGCAGGAGCTGGGCGACACAGTG
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/poroduct= "cancer asscociated antigen"
                                   ----AACAGCAAGCGCTCACGGCGCGCGCAACAACGAGAACGTGAGAAC
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                                                                                                                                                                                                                                                                                                                                           2.37e-60
728.00
74.79%
58.12%
49.16%
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                                                                                                                                                                                                                                                                                                                                                                                                                                      366 G;
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Indels:
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Conservative:
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        A partial cDNA clone (AAT69651), designated ING1, codes for a tumour suppressor protein p33ING1 (AAW1918) that is a potent inhibitor of cell growth. It was isolated by subtractive hybridisation between normal mammary and transformed epithelia cDNAs, isolation of an antisense ING1 cDNA insert that caused increased cell proliferation, and use of the insert to screen normal human fibroblast and HeLa cDNA libraries. A complete I sequence (AAT6952) was obtd. by 5'RACE. ING1 is localised to 13933-34 chromosome region, to which a number of human cancers.
                                                                                                                            Claim 1; Fig 2; 63pp;
                                                                                                                                                 Isolated tumour suppressor gene, ifor inhibiting or increasing cell treatment or diagnosis of cancer
                                                                                                                                                                                                                                   Garkavstev I,
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P-PSDB; AAW19118.
                                                                                                                                                                                                                                                                                  15-NOV-1996;
08-DEC-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           diagnosis;
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                                                                                                                                                                                                                                                         (UYTE-) UNIV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tumour suppressor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene
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95US-0569721.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           therapy;
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109..741
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  used
ING1 is localised to the
mber of human cancers have
sed in the diagnosis of
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> 843 263

783

723 223 663

brain

cancer;

in particular for

epithelial

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RESULT 12
AAV62285
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XX
DE Parti
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Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Alignment Scores: Pred. No.: Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               breast cancer; a decreased level cells. They can also be used in proliferation of cancer cells.
 Partial ING1 partial cDNA sequence
                      18-JAN-1999
                                          AAV62285
                                                             AAV62285 standard; cDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1902
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                                                                                                                                                                                                                                                                                                                  CysHisMetAlaAsnGlyIleGluAspCysAspAspGlnProProLysGluLysLysSer 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LysThrMetAspLysSerThrGluLysThrLysLysAspArg
                                                                                                                                                                                            GluMetIleGlyCysAspAsnGluGlnCysProIleGluTrpPheHisPheSerCysVal
                                                                                                                                                                                                                                   GluPheAlaIleAspProAsnGluProThrTyrCysLeuCysAsnGlnValSerTyrGly
                                                                                                                                                                                                                                                              TIGGCGACGAGAAGATCCAGATCGTGAGCCAGATGGTGGAGCTGGTGGAGAACCGCACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LeuAsnGlnLysLysArgLeuGlnGlnLeuLeuGlnArgAlaLeuIleAsnSerGlnGlu
                                                                                                                                                      SerLeuThrTyrLysProLysGlyLysTrpTyrCysProLysCysArgGlyAspAsnGlu
                                                                                                                                                                                                                        AAGCCC----AACAGCAAGCGCTCACGGCGGCAGCGCAACAACGAGAACCGTGAGAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TyrGlnGluThrLeuLysGluIleAspAspValTyrGluLysTyrLysLysGluAspAsp
                                                                                                                                                                                                                                                                                                                                                                                    GGCAACAGCGGCAAGGTTGGCGCGGACAGGCCCCAATGGCGATGCGGTAGCGCAGTCTGAC
                                                                                                                                          GGGCTCAATCATAAACCCAAGGGCAAGTGGTACTGTCCCAAGTGCCGGGGGGAGAACGAG
                                                                                                                                                                                 GCGTCCAGCAACCACGACGACGACGGCGCCTCGGGCACACCCCAAGGAGAAGAAGGCC
                                                                                                                                                                                                                                                                                                                                                                                                                            CGGCAGGTGGACAGCCACGTGGAGCTGTTCGAGGCGCAGCAGCAGGAGCTGGGCGACACAGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                              ArgGlnMetGluLeuHisSerGlnCysPheGlnAspProAlaGlu-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LeuGlyAspGluLysIleGlnIleValThrGlnMetLeuGluLeuValGluAsnArgAla 115
                                                                                                    AAGACCATGGACAAAGCCCCTGGAGAAATCCAAAAAAGAGAGG
                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             B₽;
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P-PSDB; AAW79674.
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brain tumour; gene therapy; tumour suppressor; ss
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56 TyrGlnGluThrLeuLysGluIleAspAspValTyrGluLysTyrLysLysGluAspAsp
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CC performed with cDNA from normal mammary epithelial cells, and CC subtracted cDNAs were cloned into retrovirus vector pLNCX. Following passage through a packaging line, normal mouse mammary CC epithelial cells were infected, and infected cells were injected colls colls in to nude mice. Putative transforming fragments from tumours were collsolated by PCR (see AAV62290-91) and subcloned into LNCX. An ING1 cragment was obtained and used to screen normal human fibroblast collsolated collsolated collsolated in the partial ING1 sequence. The complete cDNA sequence (see CC AAV62292) was obtained by RACE. A claimed method to potentiate collsolated collsolated collsolated or an oligonucleotide encoding such as a peptide. CC alaimed method for inhibiting apoptosis in a eukaryotic cell collsolated collsolated intity in an assay for determining the apoptotic characteristics of a collsolated cell, and an isolated eukaryotic cell constantially free of p33ING1 biological activity. The invention collsolated collsolates ING1 derivatives or variants that may be used to induce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This is the nucleotide sequence of a human ING1 (INhibitor of Growth) partial cDNA clone that codes for a p133ING1 polypeptide (see AAW79674), a novel inhibitor of cell growth land a candidate tumour suppressor. ING1 is a new gene that is expressed in normal mammary epithelial cells, but which is expressed only at lower levels in several cancerous mammary epithelial cells in several cancerous mammary brain tumours. To isolate ING1, a subtractive hybridisation of breast cancer cell lines cDNAs was subtractive hybridisation of breast cancer cell line cDNAs was
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/note= "direct primer
complement (763..782)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Isolated tumour suppressor gene, ING1 - useful to develop products for inhibiting or increasing cell proliferation, in particular for treatment or diagnosis of cancer
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P-PSDB; AAW18119.
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                                                                                                                                                     GGCAACAGCGGCAAGGTTGGCGCGGACAGGCCCAATGGCGATGCGGTAGCGCAGTCTGAC
                                                                                                      CTGGGCGACGAGAAGATCCAGATCGTGAGCCAGATGGTGGAGCTGGTGGAGAACCGCACG 369
                                                                                                                  LeuGlyAspGluLysIleGlnIleValThrGlnMetLeuGluLeuValGluAsnArgAla
                                                                                                                                                                 LeuAsnGlnLysLysArgLeuGlnGlnLeuLeuGlnArgAlaLeuIleAsnSerGlnGlu
                                                        CGGCAGGTGGACAGCCACGTGGAGCTGTTCGAGGCGCAGCAGGAGCTGGGCGACACAGTG
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  This is the nucleotide sequence of a human ING1 (INhibitor of Growth) that codes for a pl33ING1 polypeptide (see AAW79675), a novel inhibitor of cell growth and a candidate tumour suppressor. ING1 is a new gene that is expressed in normal mammary epithelial cells, but which is expressed only at lower levels in several cancerous
                                                                                                      Modulating eukaryotic apoptosis by increasing p33ING1 using p33ING1 derivatives, to induce apoptosis in cano in the investigation of apoptotic pathways
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tumour; gene 1
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GluMetIleGlyCysAspAsnGluGlnCysProIleGluTrpPheHisPheSerCysVal
                           GluPheAlaIleAspProAsnGluProThrTyrCysLeuCysAsnGlnValSerTyrGly
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                                                                               This is the nucleotide sequence encoding the human p33-ING1 protein, cused in the method of the invention. The ING1 gene encodes p33-ING1 which can be used to modulate the activity of, isolate or detect p53. Expression of the ING1 and p53 genes in a mammalian cell results in cormal growth regulation anchorage dependent growth and apoptosis as a response to irreversible DNA damage and other cellular insult. Inhibition of expression of either gene results in a loss of cellular growth control, anchorage independent growth, inhibition of apoptosis and resistance to radiation and cytotoxic drugs. The p33-ING1 is a component of the p53 signalling pathway that cooperates with p53 in negative regulation of cell proliferation by modulating p53 dependent transcriptional activation. Biological function of p53 signalling pathway can therefore be regulated (both enhanced or suppressed) by by modulating p33-ING1 activity. The modulating p33-ING1 activity can
                                       be used for the stimulation or restoration of the p53 pathway anti cancer therapy or for the suppression of the p53 pathway defend sensitive tissues from genotoxic stress or for the gene
                                                                                                                                                                                                                                                                                                                                                                          WPI;
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26-SEP-1997;
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                              immortal cell lines.
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AF07835 Homo sapi
A717757 Mus muscu
AF17757 Homo sapi
A7110392 Homo sapi
AR171884 Sequence
AF044076 Homo sapi
AK167042 Sequence
AF044071 Homo sapi
AF149721 Homo sapi
AF18850 Homo sapi
AF17755 Mus muscu
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Copyright (c) 1993 - 2003 Compugen Ltd.
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1080)

Harris, C.C. and Nagashima, M.

Harris, C.C. and Nagashima, M.

Theorem suppressor gene, p471ng3

Patent: WO 0159114-A 7 16-A0G-22001;

THE SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES (US)
101 IleGlnIleValThrGlnMetLeuGluLeuValGluAsnArgAlaArgGlnMetGluLeu
                                                                                                            121 HisSerGlnCysPheGlnAspProAlaGluSerGluArgAlaSerAspLysAlaLysMet
                                                                                                                                                                 141 AspSerSerGlnProGluArgSerSerArgArgProArgArgGlnArgThrSerGluSer
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Sequence 7 from Patent W00159114.
AX211560 GI:15523814
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/db_xref="taxon:9606"
/note="p33ING2"
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NVSYLRELDNKYQETLKEIDDYYEKYKKEDDLNQKKRLQQLLQRALINSQELGDEKIO
NVSYLRELDNKYQETLKEIDDYYEKYKKEDDLNQKKRLQQLLQRALINSQELGDEKIO
TYQMLELLVENRARQMELHSQCFQDPASERRASDKAKMDSOSPERSSRRPRQRTSES
RDLCHMANGIEDCDDOPPKEKKSKAKKKRSKAQGREBASPVEFAIDPNBETYCLCN
QVSYGEMIGCDNEQCPIEWFHFSCVSLIYKPKGKWYCPKCRGDNEKTMDKSTEKTKKD
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                               Shimada, Y., Saito, A. and Horle, M.

Shimada, Y., Saito, A. and Horle, M.

Direct Submission

Submitted (07-APR-1998) Yoshikazu Shimada, Otsuka Pharmaceutical

Co. Ltd., Otsuka GEN Research Institute; Kagasuno, Kawauchi-cho,
Tokushima, Tokushima 771-0192, Japan

(E-mail:shim@otsuka.genome.ad.jp, Tel:81-886-65-2888(ex.2476),

Fax:81-886-37-1035)
                                                                                                                                    1 (sites)
Shimada,Y., Saito,A., Suzuki,M., Takahashi,E. and Horie,M.
Cloning of a novel gene (INGIL) homologous to ING1, a candidate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AspMetGlnArgAsnValSerValLeuArgGluLeuAspAsnLysTyrGlnGluThrLeu
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                                                                       Homo sapiens fetal tissue_lib:fetal-brain cDNA to mRNA.
Homo sapiens
    Homo sapiens ING1L mRNA for ING1Lp, complete cds. AB012853
                                                                                                                                                                              tumor suppressor
Cytogenet. Cell Genet. 83 (3-4), 232-235 (1998)
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/db_xref="G1:4115555"
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="4"
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/gene="ING2"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1080)
Nagashima, M., Shiseki, M., Miura, K., Hagiwara, K., Linke, S.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                   AspMetGlnArgAsnValSerValLeuArgGluLeuAspAsnLysTyrGlnGluThrLeu
                                                                                                            IleGlnIleValThrGlnMetLeuGluLeuValGluAsnArgAlaArgGlnMetGluLeu
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                                                                   SerArgLeuLeuThrCysTyrValGlnAspTyrLeuGluCysValGluSerLeuProHis
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                                  MetLeuGlyGlnGlnGlnGlnGlnLeuTyrSerSerAlaAlaLeuLeuThrGlyGluArg
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Homo sapiens p33 (ING2) mRNA, complete cds.
AF053537
  Gaps:
                 US-09-513-365A-1 (1-280) x AX211560 (1-1080)
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NVSVLRELDNKYQETLKEIDDYYEKYKKEDDLNQKKRLQQLLQRALINSQELGDEKIQ IVTQMLELYENRARQMELHSQCFQDPAESBRASDKAKMDSSQPERSSRRPRRQRTSES BLOCHMANGIEDCDDQPPKEKKSKSKKKRSKAKQEREASPVEFAIDPNEPTYCLCN QVSYGEMIGCDNEQCPIEWFHFSCVSLTYKPKGKWYCPKCRGDNEKTMDKSTEKTKD RRSR" /translation-"MLGQQQQQLYSSAALLTGERSRLLTCYVQDYLECVESLPHDMQR 247 100 120 127 187 307 367 427 40 20 9 80 IleGlnIleValThrGlnMetLeuGluLeuValGluAsnArgAlaArgGlnMetGluLeu 41 AspMetGlnArgAsnValSerValLeuArgGluLeuAspAsnLysTyrGlnGluThrLeu LysGluIleAspAspValTyrGluLysTyrLysLysGluAspAspLeuAsnGlnLysLys ArgLeuGlnGlnLeuLeuGlnArgAlaLeuIleAsnSerGlnGluLeuGlyAspGluLys Pedeux, R., Wang, X.W., Yokota, J., Riabowol, K. and Harris, C.C. DNA damage-inducible gene p331NG2 negatively regulates cell proliferation through acetylation of p53 Proc. Natl. Acad. Sci. U.S.A. 98 (17), 9671-9676 (2001) Carcinogenesis, Bldg.37 Rm.2C01, Harris, C.C. 1080 280 0 0 0 Direct Submission Submitted (12-Marshine) Nagashima, M., Hagiwara, K., Minter, A.R. and H Direct Submission Submitted (12-MAR-1998) Laboratory of Human National Cancer Institute, 37 Convent Drive Bethesda, MD 20892, USA Conservative: Mismatches: Length: Matches: 238 Indels: 1. .1080 /organism="Homo sapiens" /db_xref="taxon:9606" /chromosome="4" /protein_id="AAG11395.1" /db_xref="G1:9992838" Gaps: (1-1080)

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Series: IRAL Plate: 15 Row:
This clone was selected for
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Tissue Procurement: DCTD/DTP
CDNA Library Preparation: Rubin Laboratory
CDNA Library Prayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gailthersburg, Maryland;
Web site: http://www.nisc.nih.gov/
Contact: nisc_mgc@ehgri.nih.gov
Akhter.N., Ayele.K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakesley,R.W., Bookstrom-Sternberg,S.M., Brinkley,C., Brooks,S.,
Blakesley,R.W., L., Granite,S., Guna,X., Gupta,J., Haghighi,P.,
Bansen,N., Ho,S.-L., Karlins,E., Laric,P., Legaspl,R., Maduro,Q.L.,
Maislello,C., Maskeri,B., Mastrian,S.D., McCloskey,J.C., McDowell,J.,
Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W., Tsurgeon,C.,
Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L., Young,A.,
Zhang,L.-H. and Green,E.D.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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National Cancer
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Submitted (07-MAY-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                  GATAATGAGAAAACAATGGACAAAAGTACTGAAAAGACAAAAAAAGGATAGAGATCGAGG
                                                                                                                                                                                                                    BCO30128 1141 bp mRNA linear PRI 20-MAY-Homo sapiens, inhibitor of growth family, member 1-like, clone MGC:10524 IMAGE:3941655, mRNA, complete cds.
HisSerGlnCysPheGlnAspProAlaGluSerGluArgAlaSerAspLysAlaLysMet
                                                               AspSerSerGlnProGluArgSerSerArgArgProArgArgGlnArgThrSerGluSer
                                                                                 LysLysSerLysSerAlaLysLysLysLysArgSerLysAlaLysGlnGluArgGluAla
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/traislation="M.GQQQQQLYSSAALLTGERSRLLTCYVQDYLECVESLPHDMQR
NVSYLRELDNKYQETLKEIDDYYEKYKREDDLNQKRRLQQLLQRALINSQELGDEKIQ
NYSYLRELDNKYQETLKEIDDYYEKYKREDDLNQKRRLQQLLQRALINSQELGDEKIQ
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QVSYGEMIGCDNEQCPIEWFHFSCVSLTYKPKGKWYCPKCRGDNEKTMDKSTEKTKKD
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This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 4504694
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                                                                                                                                                                                                                                                              /product-"inhibitor of growth family, member 1-like"
/protein_id-"AAH30128.1"
/db_xref-"GI:20987213"
                                                                                                                                                    carcinoma"
                                                        /organism="Homo sapiens"
/db_xref="LocusID 3622"
/db_xref="taxon:9606"
/clone="MGC:10524 IMAGE:3941655"
/tissue_type="Lung, small cell carc//clone_lib="NHL MGC_7"
/lab_host="DH10B-R"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length:
Matches:
Conservative:
Mismatches:
Indels:
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1 MetLeuGlyGlnGlnGlnGlnLeuTyrSerSerAlaAlaLeuLeuThrGlyGluÀrg 1	Db 181 AAGGAATTGATGATGTCTACGAAAATATAAGAAGAAGAAGAAGAAGAAA 240 Qy 81 ArgLeuGlnGlnLeuLeuGlnArgAlaLeuIleAsnSerGlnGluLeuGlyAspGluLys 100	421 GATTCCAGCCAACCAGAAGATCTTCAGAGAGGCCCCGCGGGCGCGCCGTIIIIIIIIII	Oy 221 SeTTyrGlyGluMetileGlyCysAspasnGluGlnCysProlleGluTrpPheHisPhe 240 11111111111111111111111111111111111	Mus musculus. ISM Mus musculus Eukaryota; Metazoa; Ch Manmalla; Eutheria; Ro I (bases 1 to 1001) RS Nagashima M., Hagiwara Direct Submission AL Submitted (16-JUL-1998 National Cancer Instit Convent Dr., Bldg. 37,
181 LystysSerlysSeralalysLystysRargSerLysAlaLysGlnGluargGluala 20 1111111111111111111111111111111111	ASPLYSSETTHGGGGAATGGTATTGCCCAAAGTGCAAAGTGCAAAGLGSETTHGGGGGAAATGGTATTGCCCAAAGTGCAAAGAAAAGAA	EVERTADEA; EURATYOATA MAREAZOA; CNORDATA; CTAINIACA; VETTEDEATA; EUTELEOSTOMN; MARMMALLA S. LUBERIA; Primates; Catarrhini; Hominidae; Homo. AUTHORS Cal.S., Freije.J.M. and Lopez-Otin.C. TITLE ING2.a new possible gene supressor tumor JOURNAL Unpublished REFERENCE 2 (bases 1 to 843) AUTHORS LOPEZ-Otin.C. TITLE Direct Submission JOURNAL Submitted (08-JUN-1998) Lopez-Otin C.; Bioquimica y Biologia Molecular, Universidad de Oviedo. Facultad de Medicina., C/ Julian Claveria s.fr., 33006, SPAIN FEATURES 1 843 Authors Source Location/Qualifiers Au	/tissue_type="breast tumor" gene /tissue_type="breast tumor" 1. 843	Alignment Scores: 7.87e-113 Length: 843 Pred. No.: 7.87e-113 Length: 843 Score: 1478.00 Matches: 279 Percent Similarity: 100.00% Conservative: 1 Best Local Similarity: 99.64% Mismatches: 0 Query Match: 99.80% Indels: 0 DB: 99.80% Indels: 0 US-09-513-365A-1 (1-280) x HSAJ6851 (1-843)

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HSING2S2 974 bp DNA linear PRI 08-SEP-2000 Homo sapiens p33 (ING2) gene, exon 2, complete sequence; and complete cds.

AF062748 I GI:9992841
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RRSR"
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Nagaabilma, M., Hagiwara, K., Minter, A.R. and Harris, C.C. Direct Submission
Submitted (01-MAY-1998) Laboratory of Human Carcinogenesis, National Cancer Institute, 37 Convent Dr. Bldg.37, Rm.2C26, Bethesda, MD 20892, USA
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231
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Louis,
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                                                                    Submitted (16-JAN-2002) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. MO 63108, USA
                                                                                                                                                     Submitted (10-APR-2002) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    * NOTE: This is a 'working draft' sequence. It currently consists of 8 contigs. The true order of the pleces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as * runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                               Apr 10, 2002 this sequence version replaced g1:18677601
                                                                                                                                                                                                                                                                                                                                   Sequencing vector: M13; 0% Sequencing vector: M13; 0% Sequencing vector: plaamid; 100% Chemistry: Dye-trimer ET; 0% of reads Chemistry: Dye-trimer ET; 0% of reads Chemistry: Dye-trimator Big Dye; 100% of reads Assembly program: Phrap; version 0.990319 Consensus quality: 18904b bases at least 040 Consensus quality: 190073 bases at least 020 consensus quality: 191699 bases at least 020 lineart size: 204000; agarose-fp Insert size: 105074; sum-of-contigs Quality coverage: 10.96 in 020 bases; sum-of-contigs Quality coverage: 10.96 in 020 bases; sum-of-contigs
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Waterston, R.H.
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Homo sapiens chromosome 4 clone RP11-367N14, WORKING DRAFT SEQUENCE, 8 unordered pieces.
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HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
HOMO SADIENS
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93.98%
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Query Match:
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147293 AAATGGTATTGCCCAAAGTGCAGGGGAGATAATGAGAAAACAATGGACAAAAGTACTGAA 147352
                                                                                                                                                Rattus norvegicus clone CH230-129P3, *** SEQUENCING IN PROGRESS AC128348
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Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
                                                                                           147353 AAGACAAAAAGGATAGAAGATCGAGG 147379
                                             LysThrLysLysAspArgArgSerArg 280
                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                           AC128348.1 GI:219C
HTG: HTGS_PHASE1.
Rattus norvegicus.
Rattus norvegicus
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Worley, K.C.
Direct Submission
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                                             272
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AC128348
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    212 ProThrTyrCysLeuCysAsnGlnValSerTyrGlyGluMetIleGlyCysAspAsnGlu 231
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           32 LeuGluCysValGluSerLeuProHisAspMetGlnArgAsnValSerValLeuArgGlu 51
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Matches:
Conservative:
Mismatches:
Indels:
                                      5759. .6866
/note-"assembly_name:Contig58"
6967. .37117
/note-"assembly_name:Contig65"
37218. .101402
/note-"assembly_name:Contig65
                     'note="assembly_name:Contig56"
                                                                                                                                                                                                     vector_side.left"
101503. .189972
/note="assembly_name:Contig67
                                                                                                                                                                                                                                                                           US-09-513-365A-1 (1-280) x AC107214 (1-189972)
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gap of unknown length
contig of 11439 bp in length
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of 6219 bp in length
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Rattus norvegicus"
/db_xref="taxon:10116"
/clone="CH230-12993"
35809 c 36510 g 44464 t
                                                                                                                                                                                                                                                                        contig of 4862 b
gap of unknown 1
contig of 4606 b
gap of unknown 1
                                                                        of 3298 h
unknown
                                                                                                                                                                                                                            unknown of 5139 h
                                                                                                           of 3080 lunknown
                                                                                                                                               of 4112
                                                                                                                                                                                 of 5888
                                                                                                                                                                                                  of 2671
                                                                                                                                                                                                                   of 4075
                                                                                                                                                                                                                                                       of 3444
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gap of unknown
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gap of unknown
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                                                                                                                             of 4468
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157305
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                                                                                             NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a "working draft' sequence. It currently consists of 50 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
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194
45
36
8
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Matches:
Conservative:
Mismatches:
Indels:
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Victoria, British Columbia V8W
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1 (bases 1 to 1094)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wagner, M.J., Gogela-Spehar, M., Skirrow, R.C., Johnston, R.N., Riabowol, K. and Helbing, C.C.
Expression of Novel ING Variants is Regulated by Thyroid Hormone
                                                                                                                                                                                                                                                                                                                                                                  ProLysCysArgGlyAspAsnGluLysThrMetAspLysSerThrGluLysThrLysLys
LeuGlyAspGluLysIleGlnIleValThrGlnMetLeuGluLeuValGluAsnArgAla
                                           ArgGlnMetGluLeuHisSerGlnCysPheGlnAspProAlaGluSerGluArgAlaSer
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Helbing, C.C., Wagner, M.J., Gogela-Spehar, M., Skirrow, R.C.,
Johnston, R.N. and Riabowol, K.
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J. Biol. Chem. 276 (50), 47013-47020 (2001)
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complete cds
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109. 945
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Xenopus laevis
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LOCUS
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11648: contig of 1179 11748: gap of unknown 13201: contig of 1453 13301: gap of unknown 14501: contig of 1201 14601: gap of unknown 15892: contig of 1291 15992: gap of unknown 17523: contig of 1531 17623: gap of unknown 18739: contig of 1116 18839: gap of unknown 20023: contig of 1116 18839: gap of unknown 20123: gap of unknown	of 1192 unknown of 1408 unknown of 1193 unknown of 1939 unknown of 2094 unknown of 2910 unknown of 1632	, , , , , , , , , , , , , , , , , , ,	// // // // // // // // // // // // //
	nowno sapiens chromosome 4 clone kPll-19bMD, *** PROGRESS ***, 26 unordered pieces. AC114762 AC114762 AC114762 AC114762 AC114762 HASE1. Homo sapiens Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebra Mammalia; Eutheria; Primates; Catarrhini; Homini 1 (bases 1 to 42029) Waterston, R.H. The sequence of Homo sapiens clone Unpublished 2 (bases 1 to 42029) Waterston, R.H. Direct Submission Submitted (11-MRR-2002) Genome Sequencing Center Submitted (11-MRR-2002) Genome Sequencing Center University School of Medicine, 4444 Forest Park	nter, Washington ark Parkway, St. ed gi:19339148.	Contact: submissions@watson.wustl.edu/gsc/index.shtml Contact: submissions@watson.wustl.edu

21-NOV-1999

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NASNNHBHDDITSGTPFEKRAKTRSKKKRRSGARAREASPADFPIDPNEPTYCLCNOY
SYGEMIGCDNDECPIEWFHFSCVGLNHKPKGKWYCPKCRGESEKTMDKALEKSKKERA
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Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                   Submitted (11-MAY-1999) Genome Therapeutics Corp., 100 Beaver Waltham, MA 02453, USA Location/Qualifiers
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                                                                         mRNA linear complete cds.
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Matches:
Conservative:
Mismatches:
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                                                                        AF149820
Mus musculus p33ING1 protein mRNA,
AF149820
AF149820.1 GI:6456561
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1. .840
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Mus musculus
Bukaryota; Metazoa; Chordata;
Mammalia; Butheria; Rodentia;
1 (bases 1 to 840)
                                                                                                                                                                                                Rancourt, D. and Garkavtsev, I.
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880.50
77.78%
61.48%
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2 (bases 1 to 840)
Garkavtsev,I.V.
Direct Submission
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Best Local Similarity:
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38791. .42029
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38791. .42029
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FEATURE	BASE COUNT ORIGIN Alignment Sc Pred. No.: Score: Percent Simi Best Local S Query Match: DB:	-60-sn	6 6 6 6	64 64 65 64 65 64 65 65 65 65 65 65 65 65 65 65 65 65 65
118 MetGluLeuHisSerGlnCysPheGlnAspProAlaGluSerGluArgAla 134	188 LysLysLysAgSerLysAlaLysGlnGluArg	RESULT 13 RESULT 13 BC016573 LOCUS BC016573 LOCUS BC016573 ACCESSION BC016573 ACCESSION BC016573 ACCESSION BC016573 BC016573 ACCESSION BC016573 BC016573 ACCESSION BC016573 ACCESSI	REFERENCE 1 (bases 1 to 1584) AUTHORS Strausberg, R. TITLE Direct Submission JOURNAL Submitted (31-0CT-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA REMARK NIH-MGC Project URL: http://mgc.nci.nih.gov COMMENT CONTact: MGC help desk Email: cgapbs-remail.nih.gov Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys	CDNA Library Preparation: Life Technologies, Inc. CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Baylor College of Medicine Human Genome Sequencing Center Center code: BCM-HGSC Web site: http://www.hgsc.bcm.tmc.edu/cdna/ Contact: amg@bcm.tmc.edu Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Hale, S.M., Yoon, V.S., Kowis, C.R., Lawrence, S., Martin, R.G., Muzny, D.M., Richards, S., Gibbs, R.A. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 35 Row: i Column: 6.

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                                                                                  SerSerArgArgProArgArgGlnArgThrSerGluSerArgAspLeuCysHisMetAla 167
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 840)
                                                                                                                                                                                                                                                                                                     GlyGluArgSerArgLeuLeuThrCysTyrValGlnAspTyrLeuGluCysValGluSer
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                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mummalla; Eutherlat; Rodentla; Sciurognathi; Muridae; Murinae; Mus. 1 (2817)
Zeremski,M., Hill,J.E., Kwek,S.S., Grigorian,I.A., Gurova,K.V., Sarakavey,I.V., Diatchenko,L., Koonin,E.V. and Gudkov,A.V.
Structure and regulation of the mouse ingl gene. Three alternative transcripts encode two phd finger proteins that have opposite
                                                                                            CysAspAsnGluGlnCysProIleGluTrpPheHisPheSerCysValSerLeuThrTyr 247
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ZeremsKi,M., Hill,J., Garkavtsev,I.V. and Diatchenko,L.
Direct Submission
Submitted(16-AUG-1999) Molecular Genetics, Univ. of Illinois at
Chicago, 900 South Ashland Ave., Chicago, IL 60607, USA
                                                                                                                                                  248 LysProLysGlyLysTrpTyrCysProLysCysArgGlyAspAsnGluLysThrMetAsp
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J. Biol. Chem. 274 (45), 32172-32181 (1999)
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Mismatches:
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TRQVDSHVELFEAQQELGDTAGNSGKAGADRPKGEAAAQADKPNSKRSRRQRNNENRE
NAȘSNHDHDDGASGTPKEKKAKTSKKKRSKAKAEREASPADLPIDPNEPTYCLCNQV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       118 MetGluLeuHisSerGlnCysPheGlnAspProAlaGlu---SerGluArgAlaSerAsp 136
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Nagasalima, W., Hagiwara, K., Hancock, A.R. and Harris, C.C.
Nagasalima, M., Hagiwara, K., Hancock, A.R. and Harris, C.C.
Submitted (16-JUL-1998) Laboratory of Human Carcinogenesis,
National Cancer Institute, National Institutes of Health, 37
Convent Dr., Bldg. 37, Rm. 2001, Bethesda, MD 20892, USA
Location/Qualifiers
Nagashima,M., Shiseki,M., Miura,K., Hagiwara,K., Linke,S.P., Pedeux,R., Wang,X.W., Yokota,J., Rlabowol,K. and Harris,C.C. DNA damage-inducible gene p331NG2 negatively regulates cell prolliferation through acetylation of p53 Proc. Natl. Acad. Sci. U.S.A. 98 (17), 9671-9676 (2001) 21396501
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Mismatches:
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/db_xref="taxon:9606"
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59.26%
57.63%
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PUBMED
REFERENCE
AUTHORS
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          AUTHORS
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Search completed: June 20, 2003, 03:27:45 Job time: 2265 secs

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Sequence 17, Appl
Sequence 37, Appl
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Sequence 6, Application US/09601478

Sequence 6, Application US/09601478

Fatent No. 640378:
GENERAL INFORMATION:
TILE OF INVENTION: Human TSC403 gene and human INGIL gene
FILE REFERENCE: 060193

CURRENT FILING DATE: 2000-08-03

PRIOR PLING DATE: 1998-04-28

PRIOR APPLICATION NUMBER: JP H10-134679

PRIOR APPLICATION NUMBER: JP H10-73234

PRIOR APPLICATION NUMBER: JP H10-73234

PRIOR RILING DATE: 1998-03-05

PRIOR FILING DATE: 1998-03-05

PRIOR FILING DATE: 1998-02-03
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Conservative:
Mismatches:
Indels:
US-09-499-082-9
US-09-258-372-9
US-09-0159-871-1
US-09-0159-871-1
US-09-0159-88-2
US-09-109-286-2
US-09-109-286-2
US-09-109-286-3
US-09-370-838-146
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SOFTWARE: Patentin Ver. 2.1
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Best Local Similarity:
    Alignment Scores:
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LENGTH: 840
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/cgn2_6/ptodata/1/ina/6A_COMB.seq:*
/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/PcTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/pcTuS_COMB.seq:*
                  GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd
                                                                             nucleic search, using frame_plus_p2n model
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US-08-751-230-9
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Fgapop 6.0 , Fgapext
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seq length: 200000000
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MetLeuGlyGlnGlnGlnGlnGlnLeuTyrSerSeralaalaLeuLeuThrGlyGluarg 20	LysGlulleAspaspValTyrGluLysTyrLysLysGluAspaspLeudsnGlnLysLys LysGlulleAspaspValTyrGluLysTyrLysLysGluAspaspLeudsnGlnLysLys 		LysLysSerLysSerAlaLysLysLysArgSerLysAlaLysGlnGluArgGluAla AGAAATCCAAGTCAAGAAAAAAAAAAACGCTCCAAGGCCAAGCAAG	19
0y 1 0y 21 0y 61 0y 41		0y 121 0y 121 0b 361 0y 141 0b 421 0b 481	•	OY 201 ASPABICAL DD 781 GATAATGA 781 GATAATGA 781 GATAATGA 56-09-601-478-7 Sequence 7, Applicat 5 Patent No. 6403785; GENERAL INFORMATION: APPLICANT: OSTUKA 771LE OF INVENTYON: FILE REFERENCE: OG CURRENT APPLICATION NOT PRIOR APPLICATION NOT PRIOR FILING DATE: DATE 500 DATE: PRIOR FILING DATE: PRIOR FILING DATE: DATE 500 DATE: PRIOR FILING DATE: DATE 500 DATE: DATE 500 DATE: DATE 500

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                             brain cDNA library
                                                            Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                13-365A-1 (1-280) x US-09-601-478-7 (1-1078)
                             embryonic
                                                           4.78e-156
1481.00
100.00%
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2.1
                         TURE:
ER INFORMATION: human
PatentIn Ver.
                    sapiens
                                  E/KEY: CDS
ATION: (92)..(931)
01-478-7
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uSerGluArgAlaSerAspLysAlaLysMetAspSerSerGlnProGluArgSerSerAr
                                                                 547 AAGTGAACGAGCCTCAGATAAAGCAAAGATGGATTCCAGCCAACCAGAAAGATCTTCAAG
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                                                                                           gArgProArgArgGlnArgThrSerGluSerArgAspLeuCysHisMetAlaAsnGlyIl
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STREET: 300 South Wacker Drive.
CITY: Chicago
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Ve
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         UMBER: US/09/006,783A
15-JAN-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 4, Application US/09006783A Patent No. 6297366 GENERAL INFORMATION:
APPLICANT: Gudkov, Andrey V
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REGISTRATION NUMBER: 35,303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: p33/ING1
TITLE OF INVENTION: Pathway
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION: 312-913-0001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Garkavstev, Ig
APPLICANT: Riabowol, Karl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 873 base pairs
TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: Illinois
COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
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OTHER INFORMATION: Incyte ID No. 6426186 197886.1CB1
NAME/KEY: unsure
LOCATION: 17-37
OTHER INFORMATION: a, t, c, g, or other
                                                                                                                                                                                                                                                                                                                                                                                                 Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-513-365A-1 (1-280) x US-09-484-970B-81 (1-1154)
                                                                                                              APPLICANT: Jones, Karen A.
APPLICANT: JONES, Karen A.
APPLICANT: Wolkmuth, Wayne
APPLICANT: Walker, Michael G.
TITLE OF INVENTION: BONE REMODELING GENES
FILE REFERENCE: PB-0014 US
CURRENT APPLICATION NUMBER: US/09/484,970B
CURRENT FILING DATE: 12000-01-18
NUMBER OF SEQ ID NOS: 172
SOFTWARE: PERL Program
SEQ ID NO 81
SEQ ID NO 81
                                                              US-09-484-970B-81; Sequence 81, Application US/09484970B; Patent No. 6426186
                                                                                                                                                                                                                                                                                                                                                                                   1.34e-139
1334.00
81.87%
81.57%
90.07%
                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Homo sapiens
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Best Local Similarity:
Query Match:
DB:
                                                                                                     GENERAL INFORMATION:
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GTGGACAGCCACGTGGGCGCACCAGGAGCTGGGCGACACAGTGGGCAAC 381
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                                                                                                                                                                                                     25 GGGGAGCACCTCCACCTGGTGAAC---TATGTGGAGGACTACCTGGACTCCATCGAGTCC 81
                                                                                                                                                                                                                                LeuProHisAspMetGlnArgAsnValSerValLeuArgGluLeuAspAsnLysTyrGln 57
                                                                                                                                                                                        GlyGluArgSerArgLeuLeuThrCysTyrValGlnAspTyrLeuGluCysValGluSer 37
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Indels:
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853.50
75.74%
59.19%
    single
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             linear
                                                                                                               Percent Similarity:
Best Local Similarity:
STRANDEDNESS:
TOPOLOGY: line
MOLECULE TYPE: C
                                         ; NAME/KEY:
; LOCATION:
US-09-006-783A-4
                                                                                   Alignment Scores:
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                                 FEATURE
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LeuGlyAspGluLysIleGlnIleValThrGlnMetLeuGluLeuValGluAsnArgAla 115
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                                                                                                       DNA SEQUENCE ENCODING A TUMOR SUPPRESSOR GENE
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Mismatches:
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                                                                                                                                    STREET: Burns, Doane, Swecker & Mathis STREET: P.O. Box 1404
CITY: Alexandria STATE: Vireir
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION UNDBER:
FILING DATE: 08-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: MOOI, Leslie A.
REGISTRATION NUMBER: 37,047
REFERENCE/DOCKET NUMBER: 028722-128
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/258,257
                Sequence 1, Application US/09258257 Patent No. 5965398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                  APPLICANT: GARKAVTSEV, IGOR APPLICANT: RIABOWOL, Karl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (650) 854-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (650) 854-8275
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1902 base pairs
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74.79%
58.12%
                                                                                                                                                                                                                                  STATE: Virginia
COUNTRY: United States
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                                                                                                   TITLE OF INVENTION: DNA TITLE OF INVENTION: SUP NUMBER OF SEQUENCES: 12 CORRESPONDENCE ADDRESS: ADDRESSEE: Burns, Doa STREET: P.O. BOX 1404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: single
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                                                   GENERAL INFORMATION:
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LOCATION:
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DB:
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TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                             MOLECULE TYPE: CDNA FEATURE:
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                                --SerGluArgAlaSerAspLysAlaLysMetAspSerSer
                                                                                   GlnProGluArgSerSerArgArgProArgArgGlnArgThrSerGluSerArgAspLeu
                                                                                                    385 GCGTCCAGCAACCACGACCACGACGACGCGCCTCGGGCACACCCCAAGGAGAAGGCC
                                                                                                                                                                                              LysSerAlaLysLysLysLysArgSerLysAlaLysGlnGluArgGluAlaSerProVal
                                                                                                                                                                                                             204 GluPheAlalleAspProAsnGluProThrTyrCysLeuCysAsnGlnValSerTyrGly
                                                                                                                                                                                                                                                                224 GluMetIleGlyCysAspAsnGluGlnCysProIleGluTrpPheHisPheSerCysVal
                                                                                                                                                                                                                                                                                                                   625 GGGCTCAATCATAAACCCAAGGCAAGTGGTACTGTCCCAAGTGTCGGGGGGAGAACGAG
                                                          271 GGCAACAGCGCAAGGTTGGCGGCGGACAGGCCCAATGGCGATGCGGTAGCGCAGTCTGAC
                                                                                                                                        164 CysHisMetAlaAsnGlyIleGluAspCysAspAspGlnProProLysGluLysLysSer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1, Application US/09258371
Patent No. 5986078
GENERAL INFORMATION:
APPLICANT: Garkavtsev, Igor
APPLICANT: Riabowol, Karl
TITLE OF INVENTION: SUPPRESSOR GENE INGI
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA

ZIP: 2231-1404

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/258,371
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Burns, Doane, Swecker & Mathis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           028722-144
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/751,230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                37,047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854-7400
TELEFAX: 415-854-8275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Burns, Doane, S
STREET: 699 Prince Street
CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Mooi, Leslie A. REGISTRATION NUMBER: 37, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1902 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-258-371-1
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                                                                                                                                                                                                                                       76 LeuAsnGlnLysLysArgLeuGlnGlnLeuLeuGlnArgAlaLeuIleAsnSerGlnGlu
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                                                                         1902
136
39
45
14
                                                                                                         Conservative:
Mismatches:
                                                                                                                                                                                   US-09-513-365A-1 (1-280) x US-09-258-371-1 (1-1902)
                                                                          Length:
Matches:
                                                                                                                                        Indels:
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; Sequence 1, Application US/08569
; Patent No. 6037121
Patent No. 6037121
APPLICANT: GARKAVTSEV, Igor
                                                                      1.2e-71
728.00
74.79%
58.12%
49.16%
             109..741
                                                                                                         Percent Similarity:
Best Local Similarity:
                                                             Alignment Scores:
NAME/KEY:
              ; LOCATION:
US-09-258-371-1
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204 GluPheAlaIleAspProAsnGluProThrTyrCysLeuCysAsnGlnValSerTyrGly 223
      164 CysHisMetAlaAsnGlyIleGluAspCysAspAspGlnProProLysGluLysLysSer 183
                                                                                 184 LysSerAlaLysLysLysArgSerLysAlaLysGlnGluArgGluAlaSerProVal 203
                                                                                                        224 GluMetIleGlyCysAspAsnGluGlnCysProIleGluTrpPheHisPheSerCysVal 243
                                                                                                                                                                                                                                                                                                                      244 SerLeuThrTyrLysProLysGlyLysTrpTyrCysProLysCysArgGlyAspAsnGlu 263
                                                                                                                                                                                                                                                                                                                                                          625 GGGCTCAATCATAAACCCAAGGGCAAGTGGTACTGTCCCAAGTGCCGGGGGGAGAACGAG 684
                                                                                                                                                                                                                                                                 385 GCGTCCAGCAACCACGACCACGACGACGCCCTCGGGCACACCCAAGGAGAAGAAGGCC
                                                                                                                                                                                     Sequence 1, Application US/08751230
Patent No. 6117633
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Garkavisev, Igor
APPLICANT: Riabowol, Karl
TITLE OF INVENTION: DNA SEQUENCE ENCODING THE TUMOR
TITLE OF INVENTION: SUPPRESSOR GENE ING1
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ...orkSSEE: __ ...orkSS:
STRET: 699 Prince Street
CITY: Alexandria
STATE: VA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: MOOI, LESIIE A.
REGISTRATION NUMBER: 37,047
REFERNCE/DOCKET NUMBER: 028722-144
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/751,230
FILING DATE: 15-NOV-1996
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/569721
FILING DATE: 08-DEC-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1902 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 415-854-8275 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: . USA
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: double
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109..741
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; LOCATION:
US-08-751-230-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ||||||||:::::: ||| ::: ||||:::
211 CGGCAGGTGGACAGCCACGTGTTCGAGGCGCAGCAGGAGCTGGGCGACACAGTG 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   271 GGCAACAGGGGAAGGTTGGCGGGACAGGCCCAATGGCGATGCGGTAGCGCAGTCTGAC 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        144 GlnProGluArgSerSerArgArgProArgArgGlnArgThrSerGluSerArgAspLeu 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        56 TyrGlnGluThrLeuLysGluIleAspAspValTyrGluLysTyrLysLysGluAspAsp 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    76 LeuAsnGlnLysLysArgLeuGlnGlnLeuLeuGlnArgAlaLeuIleAsnSerGlnGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    151 CTGGGCGACGAGAAGATCCAGATCGTGAGCCAGATGGTGGAGGTGGTGGAGAACCGCACG
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                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURREMY APPLICATION DATA:
APPLICATION NUMBER: US/08/569,721A
FILING DATE: 08-DEC-1995
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Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-513-365A-1 (1-280) x US-08-569-721A-1 (1-1902)
                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Donne, Swecker & Mathis STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length:
Matches:
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    TITLE OF INVENTION: DNA SEQUENCE EN NUMBER OF SEQUENCES: 12
CORRESPONDENCES: 12
                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 514
ATORNEY/AGENT INRORMATION:
NAME: MOOJ, LESLIE A.
REGISTRATION NUMBER: 37,047
REFRENCE/DOCKET NUMBER: 0287;
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 854-7400
TELECAMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 1902 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
APPLICANT: RIABOWOL, KARI
TITLE OF INVENTION: DNA S:
TITLE OF INVENTION: SUPPR
                                                                                                                                                               STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
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74.798
58.128
49.168
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LOCATION: 109..738
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Alignment Scores:
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271 GGCAACAGCGGCAAGGTTGGCGGGCGGACAGGCCCAATGGCGAATGCGGTAGCGCAGTCTGAC 330
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                                                                                                                       211 CGGCAGGTGGACAGCCACGTGGAGCTGTTCGAGGCGCAGCAGGAGCTGGGCGACACAGTG
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AAGCCC------AACAGCAAGCGCTCACGGCGGCAGCAGCAGAGAACCGTGAGAAC
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                                                                                                                                                                                                                                      LeuGlyAspGluLysIleGlnIleValThrGlnMetLeuGluLeuValGluAsnArgAla
                                                                                                                                                                                                                                                                                            ArgGlnMetGluLeuHisSerGlnCysPheGlnAspProAlaGlu-------
                                                                                                                                                                                                                                                                                                                                                   ------SerGluArgAlaSerAspLysAlaLysMetAspSerSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SerLeuThrTyrLysProLysGlyLysTrpTyrCysProLysCysArgGlyAspAsnGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GluMetIleGlyCysAspAsnGluGlnCysProIleGluTrpPheHisPheSerCysVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            264 LysThrMetAspLysSerThrGluLysThrLysLysAspArg 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Helbing, Caren C.
APPLICANT: Riabowol, Karl
APPLICANT: Johnston, Randall N.
APPLICANT: Gardavtsev, Igor
TITLE OF INVENTION: METHODS OF MODULATING APOPTOSIS
NUMBER OF SEQUENCES: 23
                             Conservative:
Mismatches:
                                                                                            US-09-513-365A-1 (1-280) x US-08-751-230-1 (1-1902)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3: Burns, Doane, Swecker & Mathis
699 Prince Street
               Matches:
                                                        Indels:
  Length:
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Patent No. 6143522
             728.00
74.79%
58.12%
49.16%
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CITY: Alexandria
                          Percent Similarity:
Best Local Similarity:
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211 CGCCAGGTGGACCACGTGGAGCTGTTCGAGGCGCAGCAGCAGGAGCTGGGCGACACAGTG 270
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LeuAsnGlnLysLysArgLeuGlnGlnLeuLeuGlnArgAlaLeuIleAsnSerGlnGlu 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       271 GGCAACAGGGGCAAGGTTGGGGGGGGAAGGCGGATGCGGTAGCGGAGTCTGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           56 TyrGlnGluThrLeuLysGluIleAspAspValTyrGluLysTyrLysLysGluAspAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            331 AAGCCC-----AACAGCAAGCGCTCACGGCGCGCGCGCAACAACGAGAACCGTGAGAAC
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136
39
45
14
                                                              OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                               NAME: MOO1, Leslie A.
REGISTRATION NUMBER: 37,047
REFERENCE/DOCKET NUMBER: 028722-148
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-854-7400
TELEPRAX: 650-854-7400
                                                                                                                                                            PRICE APPLICATION DATA:
APPLICATION NUMBER: US/08/828,158
FILING DATE: 27-MAR-1997
APPLICATION NUMBER: US 08/751230
FILING DATE: 15-NOV-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/569721
FILING DATE: 08-DEC-1995
ATTORNEY, AGENT INFORMATION:
                                                                                                               APPLICATION NUMBER: US/09/499,082 FILING DATE: CLASSIFICATION:
                               E: Floppy disk
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 1902 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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74.79%
58.12%
49.16%
ZIP: 22313-1404
COMPUTER READABLE FORM:
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Best Local Similarity:
                               MEDIUM TYPE:
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US-09-499-082-1
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Score: 728.00 Matches: 136 Percent Similarity: 74.79% Conservative: 39 Best Local Similarity: 58.12% Mismatches: 45 Query Match: 49.16% Indels: 2 DB: 4 Gaps: 2	56 TyrGludluThrLeuLysGlulleAspAspValTyrGluLysTyrLysLysGluAspAsp :::::::::::: : ::	70 Leuksintaysatysatytenturinenteusintayatateuteusinteit 	Db 151 CTGGGCGACGAGAAGATCGTGAGCCAGATGGTGGAGCTGGAGAGACCGCACG 210 Qy 116 ArgGlnMetGluLeuHisSerGlnCysPheGlnAspProAlaGlu130	131SerGluargalaSeraspLysalaLysMetaspSerSer 131SerGluargalaSeraspLysalaLysMetaspSerSer 131 GGCAACAGGGCAAGGTTGGGGGACAGGCCCAATGGGGATGGGGTAGGGGTAGGGGATGGGATGGGATGGGGATGGGGATGGGATGGGGATGGGGATGGGGATGGGGATGGGGATGGGATGGGGATGGGGATGGGATGGGATGGGATGGGATGGGATGGGATGGGATGGGATGGGATGGGATGGGATGGGATGGGATGGGATGGGATGGATGAGATGGGATGGATGGGATGGATGGATGGATGGATGGATGGATGGATGGATGGATGGATGGATGAT	Db . 331 AAGCCCAACAGCAGCGCGCAGCGCGCAACGAGAACGGGAACGGGAACGGGGGG	Oy 164 CysHisMetAlaAsnGlyIleGluAspCysAspAspGlnProProLysGluLysLysSer 183 ::: :::	OY 184 LysSerAlaLysLysLysArgSerLysAlaLysGlnGluArgGluAlaSerProVal 203	Oy 204 GluPhealaileaspProAsnGluProThrTyrCysLeuCysAsnGlnValSerTyrGly 223 ::	0y 224 GluMetileGlyCysAspasnGluGlnCysProileGluTrpPheHisPheSerCysVal:243	Oy 244 SerLeuThrTyrLysProLysGlyLysTrpTyrCysProLysCysArgGlyAspAsnGlu 263	Oy 264 LysThrMetAspLysSerThrCluLysThrLysLysAsparg 277	RESULT 11 US-09-258-371-9 ; Sequence 9, Application US/09258371 ; Patent No. 5986078 ; GENERAL INFORMATION: ; APPLICANT: GARYAVESV, IGOR ; APPLICANT: Riabowol, Karl ; TITLE OF INVENTION: DA SEQUENCE ENCODING THE TUMOR	; TITLE OF INVENTION: SUPPRESSOR GENE ING1 ; NUMBER OF SEQUENCES: 23 ; CORRESPONDENCE ADDRESS: ; ADDRESSEE: Burns, Doane, Swecker & Mathis ; STREET: 699 Prince Street ; CITY: Alexandria	STATE: COUNTRY: ZIP: 22
Db 385 GCGTCCAGCAACCACGACCACGACGCGCCTCGGGCACACCCAAGGAGAAGAAGACC 444 Qy 184 LysSerAlaLysLysLysLysArgSerLysAlaLysGlnGluArgGluAlaSerProVal 203	Oy 204 GluPhealaileAspProAsnGluProThrTyrCysLeuCysAsnGlnValSerTyrGly 223 :::	Db 565 GAGATGATCGCTGCGACAACGACGAGGCCCCATCGATCTCTTCTTCTTCTTCTTTTTTTT	Oy 264 LysThrWetAspLysSerThrGluLysThrLysLysAspArg 277 	RESULT 10 18.09.19.28.372-1 5 Sequence 1, Application US/09258372 5 Patent No. 6238918 6 CREMATION: 6 CREMATION: 7 CREMATI	HAPLICANT: Riabowol, Karl TITLE OF INVENTION: SUPPRESSOR GENE ING1 TITLE OF INVENTION: SUPPRESSOR GENE ING1	≌	Z 6	# E E E	H	CLASSIFICATION: PRIOR APPLICATION DATA: PRIOR APPLICATION NUMBER: 08/751,230 FILING DATE:	HTTORNEY/AGENT INFORMATION: NAME: Mooi, Leslie A. REGISTRATION NUMBER: 37,047 REPERBENE/DOCKET NIMBER: 078722-144	CATION INFORMATIC 1. 415-834-7400 1. 415-834-7400 OR SEQ ID NO: 1: 1902 base pairs cleic acid ESS: double)	Alignment Scores: 1.2e-71 Length: 1902

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244 SerLeuThrTyrLysProLysGlyLysTrpTyrCysProLysCysArgGlyAspAsnGlu 263
                                                                                                204 GluPheAlaIleAspProAsnGluProThrTyrCysLeuCysAsnGlnValSerTyrGly
                                                                            GluMetIleGlyCysAspAsnGluGlnCysProIleGluTrpPheHisPheSerCysVal
                                                                                                                                                                                                                                      277
                                                                                                                                                                                                                                                           Sequence 9, Application US/08751230
Patent No. 6117633
GENERAL INFORMATION:
APPLICANT: Garkavisev, Igor
APPLICANT: Riabowol, Karl
TITLE OF INVENTION: DNA SEQUENCE ENCODING THE TUMOR
TITLE OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                    264 LysThrMetAspLysSerThrGluLysThrLysLysAspArg
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Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: 699 Prince Street
CITY: Alexandria
STATE: VA
COUNTRY: USA
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Matches:
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APPLICATION NUMBER: US/08/751,230
FILING DATE: 15-NOV-1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/569721
FILING DATE: 08-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: MOOI, Leslie A.
REGISTRATION NUMBER: 37,047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TELECOMMUNICATION INFORMATION
TELEPHONE: 415-854-7400
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728.00
74.79$
58.12$
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
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LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             310 CTGGGCGACGAGAAGATCCAGATCGTGAGCCAGATGGTGGAGCTGGTGGAGAACCGCACG 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ||||||||::::||:: ||| ::: |||:::
370 CGGCAGGTGGACAGCCACGTGTTCGAGGCGCAGAGGAGGCTGGCGACACAGTG 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     --SerGluArgAlaSerAspLysAlaLysMetAspSerSer 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GlnProGluArgSerSerArgArgProArgArgGlnArgThrSerGluSerArgAspLeu 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -- AACAGCAAGCGCTCACGGCGGCAGCGAACAACGAGAACCGTGAGAAC 543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CysHisMetAlaAsnGlyIleGluAspCysAspAspGlnProProLysGluLysLysSer 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LysSeralaLysLysLysLysArgSerLysAlaLysGlnGluArgGluAlaSerProval 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            76 LeuAsnGlnLysLysArgLeuGlnGlnLeuLeuGlnArgAlaLeuIleAsnSerGlnGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        430 GGCAACAGCGGCAAGGTTGGCGGCGGACAGGCCCAATGGCGATGCGGTAGCGCAGTCTGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  544 GCGTCCAGCAACCACGACGACGACGCGCGCCTCGGGCACACCCAAGGAGAAGAAGGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      116 ArgGlnMetGluLeuHisSerGlnCysPheGlnAspProAlaGlu-----
              TYPE: Floppy disk
ER: IBM PC compatible
ING SYSTEM: PC-DOS/MS-DOS
RE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative:
Mismatches:
Indels:
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Matches:
                                                                                                                                                                                                                                                                                              028722-144
                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/258,371
                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/751,230
                                                                                                                                                                                                           FILING DATE:
ATORNEY/AGENT INFORMATION:
NAME: MOOI, LESIDE A.
REGISTRATION NUMBER: 37,047
REFERENCE/DOCKET NUMBER: 0287
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854-7400
TELEFAX: 415-854-8275
                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 9: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 2061 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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74.798
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490 AAGCCC----
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Best Local Similarity:
Query Match:
                                                                                                                                                        CLASSIFICATION:
                                                                                                                                   FILING DATE:
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Pred. No.:
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APPLICATION NUMBER: US/09/499,082
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; LOCATION:
US-09-499-082-9
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                                                                                                                                                                                                                                                                                                                                                             GluMetIleGlyCysAspAsnGluGlnCysProIleGluTrpPheHisPheSerCysVal
          TyrGlnGluThrLeuLysGluIleAspAspValTyrGluLysTyrLysLysGluAspAsp
                                                LeuAsnGlnLysLysArgLeuGlnGlnLeuLeuGlnArgAlaLeuIleAsnSerGlnGlu
                                                                                                                           ArgGlnMetGluLeuHisSerGlnCysPheGlnAspProAlaGlu-------
                                                                                                                                                                 -----SerGluArgAlaSerAspLysAlaLysMetAspSerSer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 9. Application US/09499082;
Patent No. 6143522;
GENERAL INFORMATION:
APPLICANT: Helbing, Caren C.
APPLICANT: Riabowol, Karl
APPLICANT: Garkavtsev, Igor
TILLE OF INVENTION: METHODS OF MODULATING APOPTOSIS;
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
                                                                                                                                                                                                                                                                                                                                                                                                                                          LysThrMetAspLysSerThrGluLysThrLysLysAspArg 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: PC_DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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Mismatches:
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CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
FILING DATE: 27-WAR-1997
APPLICATION NUMBER: US 08/751230
FILING DATE: 15-NOV-1996
FILING DATE: 15-NOV-1996
FILING DATE: 15-NOV-1996
FILING DATE: 10-NOV-1996
FILING DATE: 10-NOV-1996
APPLICATION NUMBER: US 08/569721
FILING DATE: 08-DEC-1995
ATTORNEY AGENT INFORMATION:
REFERENCE/DOCKET NUMBER: 37,047
REFERENCE/DOCKET NUMBER: 028722-148
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION INFORMA
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Best Local Similarity:
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96 LeuGlyAspGluLysIleGlnIleValThrGlnMetLeuGluLeuValGluAsnArgAla 115
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GACCTCCCCATCGACCCCAACGAACCCACGTACTGTGTGCAACCAGGTCTCTATGG
                                                                                  56 TyrGlnGluThrLeuLysGluIleAspAspValTyrGluLysTyrLysLysGluAspAsp
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Patent No. 6420136

GENERAL INFORMATION:
APPLICANT: RIABOWOL, Karl T.
TITLE OF INVENTION: METHOD OF MODULATING P53 ACTIVITY
FILE REFERENCE: 028722-181

CURRENT APPLICATION NUMBER: 02809-24

PRIOR FILING DATE: 1998-09-24

PRIOR FILING DATE: 1997-09-26

PRIOR APPLICATION NUMBER: US 60/006,783

PRIOR FILING DATE: 1998-01-14
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SOFTWARE: Patentin Ver.
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; LOCATION: (16)..(897)
US-09-159-871-1
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ORGANISM: Human
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244 SerLeuThrTyrLysProLysGlyLysTrpTyrCysProLysCysArgGlyAspAsnGlu 263
                                               GluMetIleGlyCysAspAsnGluGlnCysProlleGluTrpPheHisPheSerCysVal
                                                                                                                                  264 LysThrMetAspLysSerThrGluLysThrLysLysAspArg 277
                                                                                                                                                                                                   APPLICANT: Garkartsev, Igor
APPLICANT: Riabowol, Karl
TITLE OF INVENTION: DNA SEQUENCE ENCODING THE TUMOR
TITLE OF INVENTION: SUPPRESSOR GENE ING1
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, Doane, Swecker & Mathis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC| COMPAtible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/258,372
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Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: 699 Prince Street
CITY: Alexandria
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ARDIG APPLICATION DATA:
APPLICATION NUMBER: 08/751,230
FILING DATE:
                                                                                                                                                                                                                                                                              Sequence 9, Application US/09258372
Patent No. 6238918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Mooi, Leslie A.
REGISTRATION NUMBER: 37,047
REFRENCE/DOCKET NUMBER: 0287
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854-8275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 9: SEQUENCE CHARACTERISTICS:
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74.79%
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STRANDEDNESS: double
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
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US-09-258-372-9
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US-09-258-372-9
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Length: Matches: Conservative: 3 Mismatches: 4 Indels: 1	(1-2061)	ovalfyrgluLy : :: srgcracgagee	LeuGlnArgAl	GTGCAGCGCGC	GlnMetLeuG]	CAGATGGTGGA	eGlnAspProAl :::	GAGGCGCAGCA	JAlaSerAspLy	SCCCAATGGCGA	ArgGlnArgTh	SCGGCAGCGCAA	:AspAspGlnPr	GCGTCGGGCAC	AlaLysGlnGl	GCGAAGGCGGA	TyrCysLeuCy	TACTGTCTGTG	SProlleGluTr	CCCATCGAGTG	TyrCysProLy	STACTGTCCCAA	LysThrMetAspLysSerThrGluLysThrLysLysAspArg	AAAAAAGAGAG	
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Search completed: June 20, 2003, 03:51:30 Job time: 81 secs

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Sequence 2339, Apples Sequence 86, Appl Sequence 17, Appl Sequence 14, Appl Sequence 143, Appl Sequence 143, Appl Sequence 86, Appl Sequence 86, Appl Sequence 97, Appl Sequence 97, Appl Sequence 97, Appl Sequence 106, Appl Sequence 11, Appl Seque
Sequence 2, Appli
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TITLE OF INVENTION: Human TSC403 gene and human INGIL gene
FILE REPERENCE: Q60193
CURRENT APPLICATION NUMBER: US/10/115,899
CURRENT FILING DATE: 2002-04-05
PRIOR APPLICATION NUMBER: UP H10-134679
PRIOR FILING DATE: 1908-03
PRIOR FILING DATE: 1998-04-28
PRIOR FILING DATE: 1998-04-28
PRIOR FILING DATE: 1998-04-28
PRIOR FILING DATE: 1998-03-05
PRIOR FILING DATE: 1998-03-05
PRIOR FILING DATE: 1998-03-05
PRIOR FILING DATE: 1998-03-05
PRIOR FILING DATE: 1998-02-03
NUMBER OF SEQ ID NOS: 11
SOFTWARR: PATENTIN VET: 2.1
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FEATURE:
OTHER INFORMATION: human embryonic brain cDNA library
US-10-115-899-6
US-09-968-653A-2
US-09-9168-653A-6
US-09-918-995-37033
US-10-037-270-435
US-09-954-133-146
US-09-938-973-146
US-09-938-842A-1178
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Patent No. US20020151025A1
GENERAL INFORMATION:
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Patent No. US20020151025A1
GENERAL INFORMATION:
APPLICANT: Ostuka Pharmaceutical Co., Ltd.
TITLE OF INVENTION: Human TSC403 gene and human INGIL gene
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Matches:
CURRENT APPLICATION NUMBER: US/10/115,899
CURRENT FILING DATE: 2002-04-05
PRIOR APPLICATION NUMBER: 09/601,478
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: JP H10-134679
PRIOR PILING DATE: 1998-04-28
PRIOR PILING DATE: 1998-04-28
PRIOR FILING DATE: 1998-03-05
PRIOR FILING DATE: 1998-03-05
PRIOR FILING DATE: 1998-02-03
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PATENT NOS: 11
SOFTWARE: PATENT NOS: 11
SOFTWARE: PATENT NOS: 11
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; LOCATION: (92)..(931)
US-10-115-899-7
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Best Local Similarity:
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                                                                                                                LeuProHisAspMetGlnArgAsnValSerValLeuArgGluLeuAspAsnLysTyrGln
                                                 GlyGluArgSerArgLeuLeuThrCysTyrValGlnAspTyrLeuGluCysValGluSer
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Patent No. US20020147140A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC005
CURRENT APPLICATION NUMBER: US/09/764,877
CURRENT FILING DATE: 2001-01-17
Prior application data removed - refer to PALM or file wrapper NUMBER OF SEQ ID NOS: 4031
SOFTWARE: PatentIN Ver. 2.0
SEQ ID NO 3454
                                                                                                                                                                                                                                                                                                                                                                     MetGluLeuHisSerGlnCysPheGlnAspProAlaGlu------
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                  US-09-513-365A-1 (1-280) x US-09-968-653A-4 (1-873)
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                               TCACCTGTTGAGTTTGCAATAGATCCTAATGAACCTACATACTGCTTATGCAACCAAGTG
                                                           SerTyrGlyGluMetIleGlyCysAspAsnGluGlnCysProIleGluTrpPheHisPhe
                                                                                 TITLE OF INVENTION: p33/ING1 as a Mediator of p53 Signaling Pathway
                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
STREET: 300 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
STSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
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NAME: NO. US20030073084Alnan, Kevin
REGISTRATION NUMBER: 35,303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/968,653A
FILING DATE: 01-0ct-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/006,783A
FILING DATE: 15-JAN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 97,837 TELECOMMUNICATION:
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SEQUENCE DESCRIPTION: SEQ ID NO: 4:
                                                                                                                                                                                                                                                                             Sequence 4, Application US/09968653A Publication No. US20030073084Al GENERAL INFORMATION:
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Garkavstev, Igor
Riabowol, Karl
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STATE: Illinois
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CORRESPONDENCE ADDRESS:
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                                                                                                                             US-09-513-365A-1 (1-280) x US-09-764-877-3454 (1-8487)
                                                                              Conservative:
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Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        268 LysSerThrGluLysThrLysLysAspArg 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2, Application US/09968653A Publication No. US20030073084A1 GENERAL INFORMATION: GARVOY, Andrey V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Garkavstev, Igor
Riabowol, Karl
                                                   1.93e-73
728.00
75.22%
59.13%
                   sapiens
                                                                           Percent Similarity:
Best Local Similarity:
                  ; ORGANISM: Homo US-09-764-877-3454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF
                                               Alignment Scores:
Pred. No.:
LENGIH: 8487
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                                                                                                                                                                                                                                                6352
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          TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     144 GlnProGluArgSerSerArgArgProArgArgGlnArgThrSerGluSerArgAspLeu 163
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       76 LeuAsnGlnLysLysArgLeuGlnGlnLeuLeuGlnArgAlaLeuIleAsnSerGlnGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 490 AAGCCC-----AACAGCGCTCACGGCGCGCGCCAACAACGAGAACCGTGAGAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        116 ArgGlnMetGluLeuHisSerGlnCysPheGlnAspProAlaGlu-------
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ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARRE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/968,653A
FILING DATE: 01-Oct-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2061
135
39
46
14
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APPLICATION DATA:

APPLICATION NUMBER: US/09/006,783A
FILING DATE: 15-JAN-1998
ATTORNEY/AGENT INFORMATION:

NAME: NO. US20030073084A1nan, Kevin E REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 97,837
TELECOMMUNICATION INFORMATION:

TELEPHONE: 312-913-0001
TELEPHONE: 312-913-0002
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-513-365A-1 (1-280) x US-09-968-653A-2 (1-2061)
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Indels:
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Matches:
                STREET: 300 South Wacker Drive
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                                                                                                                                         MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: single
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74.36%
57.69%
48.75%
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                                   CITY: Chicago
STATE: Illinois
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     234 ProlleGluTrpPheHisPheSerCysValSerLeuThrTyrLysProLysGlyLysTrp
                                                                                                                                                                                                                   LeuGlnArgAlaLeuIleAsnSerGlnGluLeuGlyAspGluLysIleGlnIleValThr
                                                                                                                                                                                                                                                                                       73 CAGATGGTGGAGCTGGAGAACCGCACGCGGCAGGTGGACAGCCACGTGGAGCTGTTC
                                                                                                                                                                                                                                                                                                                                                                                                 133 GAGGCGCAGCAGGAGCTGGCCGACACAGTGGGCAACAGCGGCAAGGTTGGCGGGGCAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             154 ArgGlnArgThrSerGluSerArgAspLeuCysHisMetAlaAsnGlyIleGluAspCys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             174 AspAspGlnProProLysGluLysLysSerLysSerAlaLysLysLysLysArgSerLys
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -SerGluArg
                                                                                                                                                                                                                                                                                                                                                                                                                                     134 AlaSerAspLysAlaLysMetAspSerSerGlnProGluArgSerSerArgArgProArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 214 TyrCysLeuCysAsnGlnValSerTyrGlyGluMetileGlyCysAspAsnGluGlnCys
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Publication No. US20030073623A1
GENERAL INFORMATION:
APPLICANT: Hyseq, Inc.
TILLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
TILLE OF INVENTION: ROOM VARIOUS CDNA LIBRARIES
FILE REFERENCE: 20411-756
                                                                                        Conservative:
                                                                                                                                                                             US-09-513-365A-1 (1-280) x US-09-968-653A-6 (1-633)
                                                                                                         Mismatches:
Indels:
                                                    Length:
Matches:
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CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR FILING DATE: 1999-01-20
NUMBER OF SEQ ID NOS: 38054
SOFTWARE: FASTED for Windows Version 3.0
                                                                                                                                             Gaps:
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                                                                    662.00
75.498
61.278
44.708
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                                                                                 Percent Similarity:
Best Local Similarity:
Query Match:
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LENGTH: 421
                                     Alignment Scores:
JS-09-968-653A-6
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                                                                                                                                                                                                                                                                                                        244 SerLeuThrTyrLysProLysGlyLysTrpTyrCysProLysCysArgGlyAspAsnGlu 263
                                                                                                           GluPhealaIjeAspProAsnGluProThrTyrCysLeuCysAsnGlnValSerTyrGly :::
                                                                                                                                                                                   :::
GACCICCCCATCGACCCCAACGAACCCACGTACTGTCTGTGCAACCCAGGTCTCCTATGGG
               CysHisMetAlaAsnGlyIleGluAspCysAspAspGlnProProLysGluLysLysSer
                                         GCGTCCAGCAACCACGACGACGACGACGCCCTCGGGCACACCCAAGGAGGAGAAGGCC
                                                                                     LysSerAlaLysLysLysArgSerLysAlaLysGlnGluArgGluAlaSerProVal
                                                                                                                                                                                                                                 GluMetIleGlyCysAspAsnGluGlnCysProlleGluTrpPheHisPheSerCysVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: p33/ING1 as a Mediator of p53 Signaling Pathway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 7
CORRESPONDENCES: 7
CORRESPONDENCES: ADDRESS:
ACCORDESSEE: McDonnell Boehnen Hulbert & Berghoff
STREET: 300 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/968,653A
FILING DATE: 01-Oct-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                       844 AAGACCATGGACAAAGCCCTGGAGAAATCCAAAAAAGAGAGG 885
                                                                                                                                                                                                                                                                                                                                                                            264 LysThrMetAspLysSerThrGluLysThrLysLysAspArg 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/006,783A
FILING DATE: 15-740-1998
ATTORNEY/AGENT INFORMATION:
NAME: NO. US20030073084Alnan, Kevin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 97,837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 0

US_09-68-653A-6

Sequence 6, Application US_0968653A

Publication No. US20030073084A1

GENERAL INFORMATION;

APPLICANT: GUAKÇOV, ANDREW V

GARKAVSTEV, IGOR

RIADÓWOL, KARÍ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: 312-913-0001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 633 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 312-913-0002
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
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COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Chicago
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FEATURE:
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Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181 LysLysSerLysSerAlaLysLysLysLysArgSerLysAlaLysGlnGluArgGluAla
                                                                                                                                                                                                                                                                                                                                                                    SerTyrGlyGluMetIleGlyCysAspAsnGluGlnCysProIleGluTrpPheHisPhe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Zhao, Olng A.
APPLICANT: Zhao, Olng A.
APPLICANT: Xue, Aidong J.
APPLICANT: Xue, Aidong J.
APPLICANT: Xue, Aidong J.
APPLICANT: Yang, Yonghong
APPLICANT: Yang, Yonghong
APPLICANT: Andy, Ping
APPLICANT: May, Yunging
APPLICANT: May, Vunging
APPLICANT: Wang, Iniming
APPLICANT: Wang, Dinwei
APPLICANT: Wang, Dinwei
APPLICANT: Wang, Dinwei
APPLICANT: Wang, Dinwei
APPLICANT: Pargonal Noruni
APPLICANT: Pargonal Radoje T.
TITLE OF INVENTION: No. US20030104529AIel Nucleic Acids and
TITLE OF INVENTION: No. US20030104529AIel Nucleic Acids and
TITLE OF INVENTION: NOUMBER: US/10/037,270
CURRENT FILING DATE: 2000-04-25
PRIOR PELLNG DATE: 2000-04-25
PRIOR FILING DATE: 2000-04-25
SEQ ID NO 435
LENGTH: 1864
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                                                                                                                                                   Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                     US-09-513-365A-1 (1-280) x US-09-918-995-37033 (1-421)
                                                                                                                         Length:
Matches:
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; Sequence 435, Application US/10037270
; Publication No. US20030104529A1
; GENERAL INFORMATION:
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                                                                     or
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474.00
90.008
85.008
32.018
                                                    ; LOCATION: (1)...(421)
; OTHER INFORMATION: n = A,T,C
US-09-918-995-37033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Tang, Y. Tom
APPLICANT: Asundi, Vinod
APPLICANT: Asundi, Vinod
APPLICANT: Zhang, Jie
APPLICANT: Chen, Feiyan
APPLICANT: Chen, Rui-hong
APPLICANT: Chen, Rui-hong
APPLICANT: Xue, Aidong J.
APPLICANT: Yang, Yonghong
APPLICANT: Yang, Yonghong
APPLICANT: Zhou, Ping
APPLICANT: Zhou, Ping
APPLICANT: Zhou, Ping
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
                                         NAME/KEY: misc_feature
                                                                                                                                                   Percent Similarity:
Best Local Similarity:
                                                                                                             Alignment Scores:
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GluLeuGlyAspGluLysIleGlnIleValThrGlnMetLeuGluLeuValGluAsnArg 114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    323 AAACCTGAGTGGAGGGAAGAGCAAATGGCATCCATCAAAAAGACTACTATAAAGCTTTG 382
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62 GluIleAspAspValTyrGluLysTyrLysLysGluAspAspLeuAsnGlnLysLys---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             623 CACCATACGACAACAGATCATATTCCTGAAAAGAAATTTAAATCTGAAGCTCTTCTATCC
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Matches:
Conservative:
Mismatches:
Indels:
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359.00
34.22%
22.52%
24.24%
                                                               ; LOCATION: (164)..(1420)
US-10-037-270-435
ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                                      Similarity:
                                                                                                                                                                                             Percent Similarity:
Best Local Similari
                                        NAME/KEY: CDS
LOCATION: (164
                                                                                                                                Alignment Scores:
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Oy 55 LysTyrGlnGluThrLeuLysGluIleAspAspValTyrGluLysTyrLysLysGluAsp 74	75 AspleuAsnGlnLysLysArgLeuGlnGlnLeuLeuGlnArgAlaLeuIleAsnSerGln	Oy 95 GluLeuGlyAspGluLySIleGlnIleValThrGlnMetLeuGluLeuValGluAsnArg 114	Oy 115 AlaArgGlnMetGluLeuHisSerGlnCysPheGlnAspProAlaGluSerGluArg 133	Oy 134 AlaSerAspLysAlaLysMetAspSerSerGlnPro	Oy 146GluargSerSerArgargProArgArgGlnargThrSerGluSerArgAsp 162 ::: :: :::	RESULT 10 US-09-738-973-146 ; Sequence 146, Application US/09738973	; FGLENL NO. USZUGZOLIUSSSAI ; GENERAL INFORMATION: ; APPLICANT: Reed, Steven G. ; APPLICANT: Henderson, Robert A.	; APPLICANT: Lodes, Michael J.; APPLICANT: Fling, Steven P.; APPLICANT: Mohamath, Raodoh; APPLICANT: Algate, Paul A.	; APPLICANT: Secrist, Heather ; APPLICANT: Indirias, Carol Yoseph ; APPLICANT: Benson, Darin R.	; APPLICANT: Elliot, Mark: ; APPLICANT: Mannion, Jane ; APPLICANT: Kalos, Michael D.		m	; SOFTWARE: FastSEQ for Windows Version 3.0 ; SEQ ID NO 146 ; LENGTH: 451	; TYPE: DNA ; ORGANISM: Homo sapien US-09-738-973-146	7 Length:	Percent Similarity: 70.29% machine: 29 Best Local Similarity: 49.28% Mismatches: 31 Query Match: 110% Indels: 11 DB-: 10.08 Gans: 2	-09-513-365A-1 (1-280) x US-09-738-973-146 (1-451)	Qy 35 ValGluSerLeuProHisaspMetGlnargasnValSerValLeuArgGluLeuAspasn 54 :::	LysTyrGlnGluThrLeuLysGluIleAspAspValTyrGluLysTyrLysGluAsp 	Db 77 AAATACCAAGAGATCCTGAAGGAGCTAGACGAGCGCTACGAGGACGCTTCAGTCGCGAGACA 136 Qy 75 ASpLeuAsnGlnLysLysArgLeuGlnClnLeuLeuGlnArgAlaLeuIleAsnSerGln 94
	178 ProLysGluLysLysSerAlaLysLysLysLysLysArgSerLysAlaLysGluGlu 197 178 CCGACTCACGGAGTGGAAGAGCAAAAAAAAAAAAAAAAA	Oy 198 ArgGluala	OY 201	Oy 206 AlaileAspPicAsnGluProThrTyrCysLeuCysAsnGlnValSerTyrGlyGluMet 225	Qy 226 IleGlyCysAspAsnGluGlnCysProIleGluTrpPheHisPheSerCysValSerLeu 245 :::	OY 246 ThrTyrLysProLysGlyLysTrpTyrCysProLysCys	Oy 260 GlyaspàsnglulysThimetasplysserThrGlulysThr 273	Oy 274LysLysAspargSerarg 280 Db 1463 GATTTATATAGGACTTTAAAAAGAAGAAGAAGA 1501	RESULT 9 US-09-854-133-146	Sequence 140, Application US/O9854133 ; Publication No. US20020183499A1 ; GENERAL INFORMATION:	; APPLICANT: Lodes, Michael J. ; APPLICANT: Mohamath, Raodoh ; APPLICANT: Henderson, Robert A.		; TITLE OF INVENTION: THE THERAPY AND DIAGNOSIS OF LUNG CANCER; FILE REFERENCE: 210121.475C10 ; CURRENT APPLICATION NUMBER: US/09/854,133	; CURRENT FILING DATE: 2001-05-11 ; NUMBER OF SEQ ID NOS: 735 ; SOFTWARE: FastSEQ for Windows Version 3.0 ; SPOTT NO 1145	; SEV ID NO 140 ; LENGTH: 451 ; TYPE: DNA ; OPCANTOW: Homo canion	3-146 3-146 ores:	314.00 Matches: 6 milarity: 70.29% Conservative: 2	21.20% Indels: 9 Gaps:	US-09-513-365A-1 (1-280) x US-09-854-133-146 (1-451) QY 35 ValGluSerLeuProHisAspMetGlnArgAsnValSerValLeuArgGluLeuAspAsn 54	Db 17 ATGAGICCCTGCCTTCGACTTGCAGAAATGTCTCGCTGATGCGGGAGATCGACGC 76

us-09-513-365a-1.rnpb

AACACAGAACIIGGGAAACIIGGAIGGCIIGGIIGGIIGG	; SEQ ID NO 257 ; LENGTH: 993 ; LENGTH: 993 ; TYPE: DNA ; ORGANISM: Saccharomyces cerevisiae
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RESULT 13 US-09-918-995-160	; Publication No.	47	yr 67 ; FILE REFERENCE: ; CURRENT APPLICA ; CURRENT FILING I ; PRIOR APPLICATION	77		249	; NAME/KEY: misc. ; LOCATION: (1). ; CTHER INFORMAT: ; GG 309 US-09-918-995-1604;	Alignment Scores:	369	136	429 . DB:	CT 489 Qy 27 TYEV	161 Db 59	:: .AG 549 Qy 47 SerVi	.ys 181 Db 119 CAGC	CA 609 QY 67 TYTG	Jys 188 Db 179 GCTG	Qy 86	207 Db 239 CAGA	729 Qy 104	207 Db 299	703		1e 235 Db 398 GATT	606	255 ; S ; S ; S ; S ; S ; S ; S ; S ; S ;	; APPLICANT: Olga
23.15% Mismatches: 105 17.79% Indels: 99 10 Gaps: 8	x US-09-801-368-257 (1-993)	ValGlnAspTyrLeuGluCysValGluSerLeuProHisAspMetGlnArgAsnValSer :::	ValleuargGluLeuaspasnLysTyrGlnGluThrLeuLysGluIleaspaspValTyr :::	Glulystyrlystysgluaspasp	GlnLysLysArgLeuGlnGlnLeuLeuGlnArgAlaLeuIleAsnSerGlnGluLeuGly		AspGluLysTleGlnIleValThrGlnMetLeuGluLeuValGluAsnArgAlaArgGln::: :::::::::::::::::::::::::::		TTAGAATTCCTAGAGATCGCAATCAAGAACACAGAAATTCCTAGAGGTTTAAGACTG	HisserGlnCysPheGlnAspProAlaGluSerGluArgAlaSerAsp	Geletrusackarccarccascaariscacciccarcascaactaarasaaaaagagg	LIJANGLER SANCHEN POLITION LINE TOUT LINE TO SEL THE THE THE TALL THE TOUT LINE TO SEL THE THE THE TOUT LINE THE THE THE THE THE TOUT LINE THE THE THE TOUT LINE THE THE THE THE THE TOUT LINE THE TOU	-ArgArgGlnArgThrSerGluSerArg		AspLeuCysHisMetAlaAsnGlyIleGluAspCysAspAspGlnProProLysGluLys	AACGACGCAAACTACGGAGGCAGCAGGCACGAGGCCAAGACCACACTGGTAACAACA	SerAlaLysLys	AACTCAAGAAAAAGAGCCAACGCTGCCAATACCAACAACGCCGATCCAGAGACCAAAAAA	LysLysArgSerLysAlaLysGlnGluArgGluAlaSerProValGluPheAlaIle:::	GCAAGAGAGAGTTGCCACCACAGCCGTTTCACCAAGCACTATCAGCACGGCAACTGCC	C C. C	GCCGCGCALACGIACALCIACGCGCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	AGCAACAACAGGATATCAAGACCAAAAACCAACGACTACGGCGAACCGCTCTACTGC	InValSerTyrGlyGluMetileGlyCysAspAsnGluGlnCysPro	TACTGTAACCAAGTGGCATACGGGGAAATGGTGGGGTGTGATGGCGCAGACTGTGAGCTTA	GlufipPheHisPheSerCysValSerLeuThrTyrLysProLysGlyLysTrpTyrCys	
imilarity:	513-365A-1 (1-280)	28 ValGlnAspT ::: 31 TTAAACGACA	48 ValLeuArgG ::: 91 TTACTACACG	68 GluLysTyrL ::: ::: 151 GATAAGTTCT		: 211 AATATCAACA	98 AspGluLysI ::: : 250 GAGGAGAAA	118 MetGluLeu-	310 TTAGAATTGG	121			153ArgA	490 GCCAACAGGA	162 AspLeuCysH	550 AACGACGCAA	182 LysSerLys-	610 AACTCAAGAA	□ ··	Ö				216 LeuCysAsnG	850 TACTGTAACC	236 GlurrpPheH 	256 ProLysCysArg
Best Local S Query Match: DB:	-60-SD	oy D	Oy Dp	Qy	, y	qq	Qy Db	οy	qq	oy d	3 8	g 8	οy	qq	Οy	q	δy	qq	Οÿ	අු ද	à á	3 8	; a	οy	qq	oy Og	δλ

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TION: GENES DIFFERENTIALLY EXPRESSED IN VASCULAR TISSUE ACTIVATION
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ATION NUMBER: US/10/044,090
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GCAGAGTACATCTCCACGGTGAAGACGCTGTCTCCAGACCAGCGCGTGGAGCGCTG
338
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AAGATCCAGAACGCCTACAGCAAGTGCAAGGAATACAGTGACGACAAAGTGCAGCTG 298
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                                                 eq, Inc.
TION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
TION: TEOM VARIOUS CDNA LIBRARIES
1 20411-756
ATION NUMBER: US/09/918,995
DATE: 2001-07-30
ION NUMBER: US/09/235,076
ATE: 1999-01-20
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Matches:
Conservative:
Mismatches:
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SEQ for Windows Version 3.0
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FTTGAAAGCTCCGGAGGGCGA 421
Application US/09918995
US20030073623A1
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020137081A1
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TION: n = A,T,C or G
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ORGANISM: Homo sapiens

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                                                                                                                                                                                                                                                                                                                                                                      122 SerGlnCysPheGlnAspProAlaGluSerGluArgAlaSerAspLysAlaLysMetAsp 141
                                                                                                                                                                                                                                                                                                                                                                                                                                        SerSerGlnProGluArgSerSerArgArgProArgArgGlnArgThrSerGluSerArg 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          162 AspLeuCysHisMetAlaAsnGlyIleGluAspCysAspAspGlnProProLysGluLys 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LysSerLysSerAlaLysLysLysArgSerLysAlaLysGlnGluArgGluAlaSer 201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1650 CAGCAG-----GGTGGGGAAATTATTCTGTGTGACACC-----TGCCCT----CGTGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 471, Application US/09764864
Patent No. US20020132753A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PT23
CURRENT APPLICANTE: 2001-01-17
Prior application data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 1792
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1476 AGTGGCAGTGTCCACAGTGCCTCAGGCCGGCCT------
                                                                                                                                    ; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20020137081A1 235885.5
US-10-044-090-370
                                                                                                                                                                                                                     7805
446
20
39
39
                                                                                                                                                                                                                                                     Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                                                                                                                     US-09-513-365A-1 (1-280) x US-10-044-090-370 (1-7805)
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                                                                                                                                                                                                                       Length:
Matches:
CURRENT FILING DATE: 2002-01-09
NUMBER OF SEQ ID NOS: 850
SOFTWARE: PERL Program
SEQ ID NO 370
LENGTH: 7805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ProLysCysArgGlyAsp---
                                                                                                                                                                                                              0.000267
130.50
38.60%
26.90%
8.81%
                                                                                   TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                 Percent Similarity:
Best Local Similarity:
Query Match:
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Conservative:
Mismatches:
Indels:
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LOCATION: (894)
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LOCATION: (905
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Pred. No.:
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patent No. 6403785

GENERAL INFORMATION:
APPLICATION:
TITLE OF INVENTION: Human TSC403 gene and human INGIL gene
TITLE OF INVENTION: Human TSC403 gene and human INGIL gene
FILE REFERENCE: 060193

CURRENT FALING DATE: 2000-08-03

PRIOR APPLICATION NUMBER: JP H10-134679

PRIOR APPLICATION NUMBER: JP H10-3334

PRIOR FILING DATE: 1998-04-28

PRIOR FILING DATE: 1998-03-05

PRIOR FILING DATE: 1998-03-05

PRIOR FILING DATE: 1998-02-03

NUMBER OF SEQ ID NOS: 11

SOFTWARE: Patentin Ver. 2.1
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US-08-770-379-20

US-08-770-69A-20

US-09-230-371A-20

US-09-208-742-3

US-09-208-742-3

US-09-385-982-251

US-08-956-307B-11

US-08-956-307B-11

US-09-004-731-42

US-09-032-215-46

US-09-032-215-46
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Matches 1049; Conservative
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          version 5.1.6 - 2003 Compugen Ltd.
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-09-006-783A-4
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TITLE OF INVENTION: Human TSC403 gene and human ING1L gen; FILE REFERENCE: 060193
CURRENT APPLICATION NUMBER: US/09/601,478
CURRENT FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: JP H10-134679
PRIOR FILING DATE: 1998-04-28
PRIOR FILING DATE: 1998-04-28
PRIOR FILING DATE: 1998-03-05
PRIOR PELICATION NUMBER: JP H10-3334
PRIOR FILING DATE: 1998-02-03
PRIOR FILING DATE: 1998-02-03
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; OTHER INFORMATION: human embryonic brain cDNA library US-09-601-478-6
                                        Score 838.4; DB 4;
Pred. No. 2.9e-210;
                                                               0; Mismatches
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Sequence 81, Application US/09484970B
Patent No. 6426186
                                       77.68;
99.98;
                                                                 Conservative
                                       Query Match
Best Local Similarity
Matches 839; Conserv
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ATAAGACTATGCAATAATTTTTAATCATTAGTATTAATGGTGTATTAAAAGTTGTTGTAC 1050
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300 South Wacker Drive
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Vers
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/006,783A
FILING DATE: 15-JAN-1998
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                   Sequence 4, Application US/09006783A
Patent No. 6297366
GENERAL INFORMATION: AdPLICANT: Gudkov, Andrey V
APPLICANT: Garkavstev, Igor
APPLICANT: Riabowol, Karl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILLING TO CLASSIFICATION: 4.5. CLASSIFICATION: 4.5. TATORNEY/AGENT INFORMATION:
NAME: NO. 6297366nan, Revin E
NAME: NO. 6297366nan, Revin E
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TELECOMMUNICATION INFORMATION
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US-09-006-783A-4
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                                                                                                                                                                                                                                                                                 FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No. 6426186 197886.1CB1
LOCATION: 17-37
                                                                                                                                                                                                                                                                                                                                                                                                                        Score 825.2; DB 4;
Pred. No. 1e-206;
0; Mismatches 18;
APPLICANT: Jones, Karen A.

APPLICANT: Volkmuth, Wayne
APPLICANT: Walker, Michael G.
TITLE OF INVENTION: BONE REMODELING GENES
FILE REFERENCE: PB-0014 US
CURRENT APPLICATION NUMBER: US/09/484,970B
CURRENT FILING DATE: 2000-01-18
NUMBER OF SEG ID NOS: 172
SEG ID NO 81
LENGTH
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al Similarity 97.9%;
836; Conservative
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                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Homo sapiens
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US-09-484-970B-81
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HAME/KEY:

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US-09-258-257-1
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                                    CCAGAGAGCACTAATTAATAGTCAAGAATTGGGAGATGAAAAAAATACAGATTGTTACACA
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STREET: P.O. Box 1404
CITY: Alexandria STATE: Virginia COUNTRY: United States
ZIP: 2213-1404
COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
SOGFWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/09/258,257
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1, Application US/09258257
Patent No. 596598
GENERAL INFORMATION:
APPLICANT: GRANAVESV, IGOR
APPLICANT: RIABOWOL, Karl
TITLE OF INVENTION: DNA SEQUENCE ENCODING A TUMOR
TITLE OF INVENTION: SUPPRESSOR GENE
TUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                            Length 1902;
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                                                                                                                                                                                                                                                                                                                                                                                           Score 183.8; DB 7
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                                                          US 08/569,721
                                                                                                                                                                                                                                                                   TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                           17.0%;
57.0%;
                             08-DEC-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08
FILING DATE: 08-DEC-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                           Query Match 17.0°
Best Local Similarity 57.0°
Matches 394; Conservative
                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: single
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                                   509 TCTTCAAGAA--GACCCCGCAGGCAGCGGACCAGTGAAAGCCGTGATTTATGTCACATGG 566
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                                                                      335 CCAACAGCAAGCGCTCACGGCGGCAGCGCAACAACGAGAACCGTGAGAACGCGTCCAGCA 394
                                                                                                                            807 ATAAACCAAAGGGGAAATGGTATTGCCCAAAGTGCAGGGGAGATAATGAGAAAAAATGG
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                                                                                                          567 CAAATGGGATTGAAGACTGTGATGATCAGCCACCTAAAGAAAAGAAATCCAAGTCAGCAA
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FILING DATA:
FILING DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1, Application US/08569721A

Sequence 1, Application US/08569721A

Patent No. 6037121

GENERAL INFORMATION:
APPLICANT: GARKAVION:
APPLICANT: RIABOWOL, Karl
ITLE OF INVENTION: SUPPRESSOR GENE
NUMBER OF SEQUENCE: 12
CORRESPONDENCE ADDRESS:
ADDRESSE: Burns, Doane, Swecker & Mathis
STAREF: P.O. Box 1404
CITY: Alexandria
STARE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               867 ACAAAAGTACTGAAAAGACAAAAAAGGATAG 897
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FILING DATE: 08-DEC-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Mooi, Leslie A.
REGISTATION UNDRER: 37,047
REFERENCE/DOCKET NUMBER: 028722-128
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (650) 854-7400
TELEFAX: (650) 854-8275
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 1902 base pairs
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DNESS: single
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                                                                                                                                      APPLICANT: Garkavtsev, Igor
APPLICANT: Rabowol, Karl
TITLE OF INVENTION: DNA SEQUENCE ENCODING THE TUMOR
TITLE OF INVENTION: SUPPRESSOR GENE ING1
NUMBER OF SEQUENCES;
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIA RELease #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/258,371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             267;
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695 ACAAAGCCCTGGAGAAATCCAAAAAAAGAGAG 725
                                                                                                                                                                                                                                                ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: 699 Prince Street
CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
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| 57.0%; Pred. No. 1.4
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APPLICATION NUMBER: 08/751,230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: MOO1, Leslie A.
REGISCRATION NUMBER: 37,047
REFRENCE/COCKET NUMBER: 0287
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854-7400
                                                                                   Sequence 1, Application US/09258371
Patent No. 5986078
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                            IBM PC|compatible
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                                                                                                                                                                                                                                                                                                                                  ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1902 base pairs
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109..741
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LOCATION:
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Best Local S
Matches 394
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                                                                PatentIn Release #1.0, Version #1.30
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Pred. No. 1.4e-38;
0; Mismatches 267;
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                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 37,047
REFERENCE/DOCKET NUMBER: 028722-144
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854-8275
CORMATION FOR SECONDARY
                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentin Release #1.0, '
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/751,230
FILING DATE: 15-NOV-1996
                                                                                                                            CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/569721
FILING DATE: 08-DEC-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                       TELEFAX: 415-854-8275
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 17.0%;
Best Local Similarity 57.0%;
Matches 394; Conservative
                                                                                                                                                                                                                                                                                                                                      LENGTH: 1902 base pairs
                                                                                                                                                                                                           NAME: Mooi, Leslie A. REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: double
   COMPUTER READABLE FORM:
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109..741
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; LOCATION:
US-08-751-230-1
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                                                 Length 1902;
                                              Score 183.8; DB 3; Length
Pred. No. 1.4e-38;
0; Mismatches 267; Indels
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Patent No. 6117633
GENERAL INFORMATION:
APPLICANT: Riabowol, Karl
TITLE OF INVENTION: DNA SEQUENCE ENCODING THE TUMOR
TITLE OF INVENTION: SUPPRESSOR GENE ING1
CORRESPONDENCE ADDRESS:
ADDRESSED: Burns, Doane, Swecker & Mathis
STREET: 699 Prince Street
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                                              Query Match 17.0%;
Best Local Similarity 57.0%;
Matches 394; Conservative
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 ; LOCATION:
US-08-569-721A-1
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                                                                                  AGGTGGACAGCCACGTGAGCTGTTCGAGGCGCAGCAGGAGCTGGGCGACACAGTGGGCA
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 95 CGCAGAAGCGGCGGATGCTGCACTGTGCAGCGCGCGCGCTGATCCGCAGCCAGGAGCTGG
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ADDRESSEE: Burns, Doane, Swecker & Mathis STREET: 699 Prince Street
CITY: Alexandria
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Patent No. 6238918
GENERAL INFORMATION:
APPLICANT: GATKAVTSEV, IGOT
APPLICANT: Riabowol, Karl
TITLE OF INVENTION: DNA SEQUENCE ENCOD:
TITLE OF INVENTION: SUPPRESSOR GENE INNUMBER OF SEQUENCES: 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DAYS: APPLICATION NUMBER: US/09/258,372
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  USA
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APPLICANT: Helbing, Caren C.
APPLICANT: Riabowol, Karl
APPLICANT: Johnston, Randall N.
APPLICANT: Garkavtsev, Igor
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM: PC_DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/499,082
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hes 267;
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699 Prince Street
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Pred. No. 1.4e-
0; Mismatches
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APPLICATION NUMBER: US/08/828,158
FILING DATE: 27-MAR-1997
APPLICATION NUMBER: US 08/751230
FILING DATE: 15-NOV-1996
PRIOR APPLICATION NUMBER: US 08/569721
FILING DATE: 08-DEC-1995
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                  STAILS.
COUNTRY: USA
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC.
PC-DOS/MS-DY
                                                                                                                                                                                                          US/09499082
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REGISTRATION NUMBER: 37,047
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-854-7400
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Conservative
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LENGTH: 1902 base pairs
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                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Do
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                                                                                                                                                                                                      Sequence 1, Application
Patent No. 6143522
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394; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
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US-09-499-082-1
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Best Local Si
Matches 394,
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                                                                                                                                                                                                                                                          Length 1902;
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0; Mismatches 267; Indels
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                                                                                                                                                                                                                                                          Score 183.8;
ATTORNEY/AGENT INFORMATION:
NAME: MOOL, LGEBLEA.
REGISTRATION NUMBER: 37,047
REFERENCE/DOCKET NUMBER: 0287
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854-7400
TELEPHONE: 415-854-7275
                                                                            INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 1902 base pairs TYPE: nucleic acid STRANDEDNESS: double
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57.0%;
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109..741
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                                                                                                                                                                                                   ; NAME/KEY:
; LOCATION:
US-09-258-372-1
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357 GAGATGAAAAATACAGATTGTTACACAAATGCTCGAATTGGTGGAAAATCGGGGCAAGAC 416
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                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
SOFTWENT APPLICATION DATA:
APPLICATION NUMBER: US/09/258,371
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 183.8; DB 2;
Pred. No. 1.4e-38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches 267;
                                                                                                                                                                                                      ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: 699 Prince Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    417 AAATGGAGTTACACTCACAGTGTTTCCAAGATC-
                                                       GENERAL INFORMATION:
APPLICANT: Garkavtsev, Igor
APPLICANT: Riabbwol, Karl
TITLE OF INVENTION: DNA SEQUENCE ENCODIN
TITLE OF INVENTION: SUPPRESSOR GENE INGI
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           028722-144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/751,230
                     Sequence 9, Application US/09258371
Patent No. 5986078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Mooi, Leslie A. REGISTRATION NUMBER: 37,047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 02
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854-7400
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57.0%;
                                                                                                                                                                                                                                                                                     COUNTRY: ....
ZIP: 22313-1404
COMPUTER READABLE FORM: ### TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 2061 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 57.08
Matches 394; Conservative
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STRANDEDNESS: double
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
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; LOCATION:
US-09-258-371-9
JS-09-258-371-9
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                                                                                      Gaps
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APPLICANT: Riabowol, Karl
APPLICANT: Johnston, Randall N.
APPLICANT: Johnston, Randall N.
APPLICANT: GARVAVLESON, IGON
TITLE OF INVENTION: METHODS OF MODULATING APOPTOSIS
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
                                                 Score 183.8; DB 3;
Pred. No. 1.4e-38;
0; Mismatches 267;
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STREET: 699 Prince Street
CITY: Alexandria
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                                                 Query Match
Best Local Similarity 57.0%;
Matches 394; Conservative
; LOCATION: 16..900
US-08-751-230-9
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COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Garkavtsev, Igor
APPLICANT: Rabowoll, Karl
TITLE OF INVENTION: SUPPRESSOR GENE ING1
NUMBER OF SEQUENCES: 23
CORRESPONDENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: 699 Prince Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: US/08/751,230
FILING DATE: 15-NOV-1996
CLASSIFICATION: 514
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APPLICATION NUMBER: US 08/569721
FILING DATE: 08-DEC-1995
ATTONEY/AGENT INFORMATION:
NAME: MOOI, LESJIE A.
REGISTRATION NUMBER: 37,047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 9, Application US/08751230 Patent No. 6117633
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TELECOMMUNICATION INFORMATION
TELEPHONE: 415-854-7400
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EDNESS: double
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687 TAGATCCTAATGAACCTACATACTGCTTATGCAACCAAGTGTCTTATGGGGAGATGATAG 746
                                                                                     674 TCGACCCCAACGAACCCACGTACTGTCTGTGCAACCAGGTCTCCTATGGGGAGATGATCG
                                                                   747 GATGTGACAATGAACAGTGTCCAATTGAATGGTTTCACTTTTCATGTGTTTCACCTTACCT
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                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Garkavtsev, Igor
APPLICANT: Riabowol, Karl
TITLE OF INVENTION: DNA SEQUENCE ENCODING THE TUMOR
TITLE OF INVENTION: SUPPRESSOR GENE ING1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Release #1.0, Version. #1.30
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                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 699 Frince Street
STATE: VA
                                                                                                                                                                                                      867 ACAAAAGTACTGAAAAAGAAAAAGGATAG 897
                                                                                                                                                                                                                                      854 ACAAAGCCCTGGAGAAATCCAAAAAAAGAGAG 884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: MOOI, Leslie A.
REGISTRATION NUMBER: 37,047
REFERENCE, POCKET NUMBER: 028722-144
TELECOMUNICATION INFORMATION:
TELEPAN: 415-854-825
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 2061 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/258,372
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IBM PC compatible YSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/751,230
                                                                                                                                                                                                                                                                                                                        Sequence 9, Application US/09258372 Patent No. 6238918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Floppy disk
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: double
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16..900
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Best Local Similarity
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; LOCATION:
US-09-258-372-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 434 ACAGCGGCAAGGTTGGCGGCGGGACAGGCCCAATGGCGATGCGGTAGCGCAGTCTGACAAGC 493
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                                                                                Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 3;
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Pred. No. 1.4e-38;
                                                                                                                                                              PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/828,158
FILING DATE: 27-MAR-1997
APPLICATION NUMBER: US 08/751230
FILING DATE: 15-NOV-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/569721
FILING DATE: 08-DEC-1995
ATTONNEY, AGENT INFORMATION:
NAME: MOOJ, LESIER A.
REGISTRATION NUMBER: 37,047
REFERENCE/DOCKET NUMBER: 028722-148
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/499,082
            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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nucleic acid
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Best Local Similarity 57.03
Matches 394; Conservative
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                                                                                                                                              CLASSIFICATION:
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                                                                                                                                    FILING DATE:
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US-09-499-082-9
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US-09-006-783A-2
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TCTTCAAGAA --GACCCCGCAGGCAGCGGACCAGTGAAAGCCGTGATTTATGTCACATGG. 566
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                                                             374 AGGIGGACAGCCACGIGGAGCIGITCGAGGCGCAGCAGGAGCIGGGCGACACAGIGGGCA
                                                                                                                                               -CTGCTGAAAGTGAACGAGCCTCAGATAAAGCAAAGATGGATTCCAGCCAACCAGAAAGA
                                                                                                                                                                      134 ACAGCGGCAAGGTTGGCGCGGACAGGCCCAATGGCGATGCGGTAGCGCAGTCTGACAAGC
                                                                                                                                                                                                            CAAATGGGATTGAAGACTGTGATGATCAGCCACCTAAAGAAAAGAAATCCAAGTCAGCAA
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                     254 CGCAGAAGCGGCGGATGCTGCACTGTGTGCAGCGCGCGCTGATCCGCAGCCAGGAGCTGG
                                               GAGATGAAAAATTACAGATTGTTACACAAATGCTCGAATTGGTGGAAAAATCGGGCAAGAC
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APPLICANT: Gudkov, Andrey V
APPLICANT: Gudkov, Igor
APPLICANT: Riabowol, Karl
TITLE OF INVENTION: p33/ING1 as a Mediator of p53
TITLE OF INVENTION: Pathway
NUMBER OF SEQUENCES: 7
NUMBER OF SEQUENCES: ADDRESS:
ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
STREET: 300 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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                                                                                               AAATGGAGTTACACTCACAGTGTTTCCAAGATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/09/006,783A
FILING DATE: 15-JAN-1998
CLASSIFICATION: 435
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Patent No. 6297366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC Compatible OPERATING SYSTEM: PC-DOS/MS-
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MEDIUM TYPE: Floppy disk
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ATTORNEY/AGENT INFORMATION:
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STATE: Illinois
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US-09-006-783A-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                      567 CAAATGGGATTGAAGACTGTGATGATCAGCCACCTAAAGAAAAGAAATCCAAGTCAGCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGAAAAAGAAACGCTCCAAGGCCAAGCAGGAAAGGGAAGCTTCACCTGTTGAGTTTGCAA
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                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                 30;
                                                                                                                                                                                                                                                                                                                                                        Length 2061;
                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                        Score 182.2; DB 4;
Pred. No. 3.7e-38;
0; Mismatches 268;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACAAAGCCCTGGAGAAATCCAAAAAAGAGAG 884
NAME: NO. 6297366nan, Kevin E
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 97,837
TELECOMUNICATION INFORMATION:
TELEPHONE: 312-913-0001
                                                                                                                                                                                                                                                                                                                                                        Query Match 16.9%;
Best Local Similarity 56.9%;
Matches 393; Conservative
                                                                                                                                                         LENGTH: 2061 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                            TELEFAX: 312-913-0002
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                       MOLECULE TYPE: CDNA
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Search completed: June 20, 2003, 02:42:11 Job time: 85 secs

Y.

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(without alignments)
8254.278 Million cell updates/sec
                                                                                                                                                                                June 20, 2003, 01:22:25; Search time 192 Seconds
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GenCore version 5.1.6 (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                 1042519 segs, 733713590 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                      OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                          IDENTITY NUC
Gapop 10:0 , Gapext 1.0
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Maximum DB seq length: 200000000
                 Copyright
                                                                                                                                                                                  Title:
Perfect score:
Sequence:
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                                                                                                                                                                                                                                                                                                                   Searched:
                                                                                                         Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:* /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:* /ptodata/1/pubpna/US10_PUBCOMB.seg

/cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:* /cgn2_6/ptodata/1/pubpna/USO8_NEW_PUB.seq:* /cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*

/cgn2_6/ptodata/1/pubpna/USO6_NEW_PUB.seq: /cgn2_6/ptodata/1/pubpna/USO6_PUBCOMB.seq: /cgn2_6/ptodata/1/pubpna/USO7_NEW_PUB.seq:

/cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seg

Published_Applications_NA:*

Database :

/cgh2_6/ptodata/1/pubpna/US09_PUBCOMB.seq: /cgh2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:

6/ptodata/1/pubpna/US09_NEW_PUB.seg:

SUMMARIES

Result No.	Score	& Query Match Length DB	ength	DB	ΔΙ	Description
П	1046	6.96	1078	12	US-10-115-899-7	Sequence 7, Appli
7	838.4	77.6	840	12	US-10-115-899-6	Sequence 6, Appli
m	378.4	35.0	421	σ	US-09-918-995-37033	Sequence 37033, A
4	237.4	22.0	873	6	US-09-968-653A-4	Sequence 4, Appli
ş	183.4	17.0	8487	10	US-09-764-877-3454	Sequence 3454, Ap
9	182.2	16.9	2061	σ	US-09-968-653A-2	Sequence 2, Appli
. 7	174.4	16.1	633	σ	US-09-968-653A-6	Sequence 6, Appli
80	91.6	8.5	1864	σ	US-10-037-270-435	32
σ	83.6	7.7	451	0	US-09-854-133-146	Sequence 146, App
10	83.6	7.7	451	10	US-09-738-973-146	Sequence 146, App
11	9.99	6.2	993	10	US-09-801-368-257	Sequence 257, App
12	62	5.7	813	σ	US-09-938-842A-1178	Sequence 1178, Ap
13	56.8	5.3	456	σ	US-09-918-995-16047	Sequence 16047, A
c 14	51.6	4.8	393	10	US-09-960-352-4582	Sequence 4582, Ap
c 15	50.8	4.7	361	10	US-09-919-580-114	Sequence 114, App
c .16	49	4.5	593	δ	US-09-871-161-262	Sequence 262, App
c 17	48.8	4.5	277	10	US-09-960-352-12673	Sequence 12673, A
18	48.4	4.5	5520	O	US-10-001-887-43	Sequence 43, Appl
c 19	48	4.4	527	6	US-10-106-698-863	· m

Sequence 90, Appl	Sequence 491, App	Sequence 708, App	Sequence 6976, Ap	Sequence 5829, Ap	Seguence 14521, A	Sequence 17652, A	Sequence 8, Appl1	Sequence 1023, Ap	Sequence 1284, Ap	Sequence 690, App	Sequence 690, App	Sequence 690, App	Sequence 338, App	Sequence 529, App		Sequence 4584, Ap	Sequence 18370, A	Sequence 1369, Ap	Sequence 1689, Ap	Sequence 1, Appli	Sequence 1, Appli	Sequence 13111, A	Sequence 1, Appli	Sequence 1, Appli	
US-10-239-676-90	US-10-066-543-491	US-09-919-580-708) US-09-960-352-6976	US-10-198-846-5829	US-09-960-352-14521	US-09-918-995-17652	US-09-998-027-8	US-10-066-543-1023	US-10-066-543-1284	US-10-025-380-690	US-09-922-217-690	US-09-833-263-690	US-09-925-300-338	US-09-764-891-529	US-10-239-676-204	US-09-960-352-4584	US-09-918-995-18370	ns-	US-10-106-698-1689	US-10-263-316-1	US-09-771-404-1	US-09-918-995-13111	US-10-338-691-1	US-09-852-067-1	US-10-066-543-396
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4.4	4.4	4.3	4.3	4.3	4.3	4.2	4.2	4.2	4.2	4.2	4.2	4.2	4.2	4.2	4.2	4.1	4.1	4.1	4.1	4.1	4.1	4.1	4.1	4.1	4.0
47.6	47.2	46.6	46.2	46.2	46	45.8	45.8	45.6	45.6	45.6	45.6	45.6	45.2	45	45	44.6	44.2	44.2	44.2	44.2	44.2	44	43.8	43.8	43.6
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ALIGNMENTS

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1 GCGGCCGCCGCCGGTGCATGTGCGGCTGCTGGATGCGGAGGCGGCGGCGACGGCGGCGGCGGATT
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                                                                 APPLICANT: Ostuka Pharmaceutical Co., Ltd.
TITLE OF INVENTION: Human TSC403 gene and human ING1L gene
FILE REFERENCE: Q60193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: human embryonic brain cDNA library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 1046; DB 12;
Pred. No. 2.3e-245;
0; Mismatches 5;
                                                                                                                            CURRENT PELLIATION NUMBER: US/10/115,899
CURRENT FILING DATE: 2002-04-05
PRIOR APPLICATION NUMBER: 09/601,478
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: JP H10-134679
PRIOR PILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: JP H10-73234
PRIOR FILING DATE: 1998-03-05
PRIOR FILING DATE: 1998-03-05
PRIOR FILING DATE: 1998-03-05
PRIOR FILING DATE: 1998-02-03
Sequence 7, Application US/10115899 Patent No. US20020151025A1
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Best Local Similarity 99.5%;
Matches 1049; Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; NAME/KEY: CDS
; LOCATION: (92)..(931)
US-10-115-899-7
                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS
                                              GENERAL INFORMATION
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LENGTH: 1
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us-09-513-365a-2.rnpb

CURRENT APPLICATION NUMBER: US/10/115,899 CURRENT FILING DATE: 2002-04-05 PRIOR APPLICATION NUMBER: 09/601,478 PRIOR FILING DATE: 1000-08-03 PRIOR FILING DATE: 1998-04-28 PRIOR PELING DATE: 1998-04-28 PRIOR FILING DATE: 1998-03-05 PRIOR FILING DATE: 1998-02-03 PRIOR FILING DATE: 1998-02-03 PRIOR FILING DATE: 1998-02-03 NUMBER OF SEQ ID NOS: 11 SOFTWARE: Patentin Ver: 2.1 SOFTWARE: Patentin Ver: 2.1 SOFTWARE: DAA ORGANISM: Homo sapiens FEAUTOR: OTHER INFORMATION: human embryonic brain cDNA library US-10-115-899-6	Ouery Match 77.6%; Score 838.4; DB 12; Length 840; Best Local Similarity 99.9%; Pred. No. 1e-194; Matches 839; Conservative 0; Mismatches 1; Indels 0; Gaps 0; Qy 68 ATGTTAGGGCAGCAGCAGCAACTGTACTCGTCGGCTGCCTTGACCGGGAGCGG 127	OY 128 AGCCGCTGCTCACCTGCTACGTGCAGACTACCTTGAGTGCGTGGAGTCGCCCCCC 187	OY 248 AAGGAAATTGATGATGTCTACGAAAATATAAGAAGAAGATGATTTAAACCAGAAGAAA 307	QY 368 ATACAGATTGTTACACAAATGCTCGAATTGGGGCAAAATGGGGTTA 427	QY 488 GATTCCAGCCAACCAGAAAGATCTTCAAGAAGACCCGCAGGCAG	Db 481 CGTGATTTATGTCACATGGGAATGGGATTGAAGATGGTCAGCCACCTAAAGAA 540 Qy 608 AAGAAATCCAAGCAAAGAAAAGAAAAGACGCCCCCAAGGGAAAGGGAAAGGGAAGGT 667 Db 541 AAGAAATCCAAGTCAGCAAAAAAAAAAAAAGAAAAGCTCCAAGGCCAAGCAAAGGAAAGCT 600	OY 668 TCACCTGTTGAGTTGCAATAGATCCTAATGAACCTACTTATGCAACCAAGTG 727
QY 121 GGAGCGGAGCCGGCTGCTCACCTGCTGCAGCTACCTTGAGTGCCTGGAGTCGCT 180 LIHIHIHIHIHIHIHIHIHIHIHIHIHIHIHIHIHIHIH	QY 421 GGAGTTACACTCACAGTGTTTCCAAGATCCTGCTGAAAGTGAACGAGCCTCAGATAAAGC 480 DD 445 GGAGTTACACTCACAGTGTTTCCAAGATCTGAAAGTGAACGAGCCTCAGATAAAGC 504 QY 481 AAAGATGGATTCCAGCAAAAGATCTTCAAGAAGACCCCGCAGGCAG	Oy 541 TGAAAGCCGTGATTTATGTCACATGGCAAATGGGATTGAAGACTGTGATGATCACCCACC	OY 661 GGAAGCTTCACCTGTTGAGTTGCAATAGATCCTAATGAACCTAACTACTATATGCAA 720	QY 781 TCACTTTCATGTTTCACTTACCTATAAACCAAAGGGGAAATGGTATTGCCCAAAGTG 840 DD	OY 901 ATCGAGGTAGTAAAGGCCATCCACATTTAAAGGGTTATTGTCTTTTATAATTGGTT 960		<pre>BESULT 2 US-10-115-899-6 ; Sequence 6, Application US/10115899 ; Patent No. US20020151025A1 ; GENERAL INFORMATION: ; APPLICANT: OSTUKA Pharmaceutical Co., Ltd. ; TITLE OF INVENTION: Human TSC403 gene and human ING1L gene ; FILE REFERENCE: Q60193</pre>

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NUMBER OF
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                                              CTTCACCTGTTGAGTTTGCAATAGATCCTAATGAACCTACATACTGCTTATGCAACCAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGTCTTATGGGGAGATGATAGGATGTGACAATGAACAGTGTCCAATTGAATGGTTTCACT
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                                                                                                                                            APPLICANT: Hyseq. Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
FILE REPERENCE: 20411-756
CURRENT APPLICATION NUMBER: US/09/2918,995
CURRENT FILING DATE: 1201-07-30
PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR PRIOR DATE: 1999-01-20
NUMBER OF SEQ ID NOS: 38054
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 37033
LENGTH: 421
                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                  DB 9;
                                                                                                                                                                                                                                                                                                                                                                                                         26;
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Pred. No. 1.4e-82;
0; Mismatches 26
                                                                                                           Sequence 37033, Application US/09918995
Publication No. US20030073623A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 4, Application US/09968653A
Publication No. US20030073084A1
GENERAL INFORMATION:
APPLICANT: Gudkov, Andrey V
Garkavstev, Igor
                                                                                                                                                                                                                                                                                                                                  ; LOCATION: (1)...(421)
; OTHER INFORMATION: D = A,T,C or G
US-09-918-995-37033
                                                                                                                                                                                                                                                                                                                                                                                 35.0%;
93.8%;
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                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                           Similarity
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Matches 394
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -------CTGCTGAAAGTGAACGAGCCTCAGATA 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                205 GTCTGTGCTGCGAGAGCTGGACAACAATATCAAGAAACGTTAAAGGAAATTGATGATGT 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 108 CTCGCTGATGCGGGAGATCGACGCGAAATACCAAGAGATCCTGAAGGAGCTAGACGAGTG 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          228 GCAGCGCGCGCTGATCGCCAGCACGAGGACGACGAGAAGATCCAGATCGTGAGCCA 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               385 AATGCTCGAATTGGTGGAAAATCGGGCAAGACAAATGGAGTTACACTCACAGTGTTTCCA 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               348 GGCGCAGCAGCAGCTGGGCGACACAGTGGGCAACAGGGGCAAGGTTGGCGCGGACAGGCC 407
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              48 CTATGTGGAGGACTACCTGGACTCCATCGAGTCCCTGCCTTTCGACTTGCAGAAATGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTACGAAAAATATAAAGAAGAAGATGATTTAAAACCAGAAGAAACGTCTACAGCAGCTTCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 145 CTACGTGCAGGACTACCTTGAGTGCGTGGAGTCGCTGCCCCACGACATGCAGGAACGT
               TITLE OF INVENTION: p33/ING1 as a Mediator of p53 Signaling Pathway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 873;
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                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff STREET: 300 South Wacker Drive CITY: Chicago
                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC red
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   291;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ш
                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/968,653A
FILING DATE: 01-0ct-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 15-JAN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 97,837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: 7.813
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: No. US20030073084Alnan,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: 312-913-0001
TELEFAX: 312-913-0002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGIH: 873 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS: single
Riabowol, Karl
                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear MOLECULE TYPE: CDNA
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Matches 462; Conservative
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                                                                  SEQUENCES:
                                                                                                                                                                                        STATE: Illinois
COUNTRY: USA
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                                                                                                                                                  715 ATGCAACCAAGTGTCTTATGGGGAGATGATAGGATGTGACAATGAACAGTGTCCAATTGA 774
                                                                                                                                                                                                                                                                                           835 AAAGTGCAGGGAGATAATGAGAAAACAATGGACAAAAGTACTGAAAAAGACAAAAAGGA 894
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                           GACCAGTGAAAGCCGTGATTTATGTCACATGGCAAATGGGATTGAAGACTGTGATGATCA 594
                                                                                                                                                                                                                                                              708 GIGGIICCACIICICGIGCGIGGGCICAAICAIAAACCCAAGGGCAAGIGGIACIGIC 767
                                                                             ATGGTTTCACTTTTCATGTTTCACTTACCTATAAACCAAAGGGGAAATGGTATTGCCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 3454, Application US/09764877

Patent No. US20020147140A1

GENERAL INFORMATION:

APPLICANT: Rosen et al.

TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PCOO5

CURRENT FILING DATE: 2001-01-17

Prior application data removed - refer to PALM or file wrapper

NUMBER OF SEQ ID NOS: 4031

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 3454

LENGTH: 8487
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Pred. No. 4e-34;
0; Mismatches 266; Indels
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Best Local Similarity 57.0%;
Matches 395; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-877-3454
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564
  505 AAGATCTTCAAGAAGACCCCGCAGGCAGGCGGACCAGTGAAAGCCGTGATTTATGTCACAT
                                                                                                                                                        5588 CAACCACGACCACGACGACGCCCTCGGGCACACCCAAGGAGAAGAAGAAGAACTC
                                                                                                                                                                                                            625 AAAGAAAAGAAACGCTCCAAGGCCAAGCGGAAAGGGAAGCTTCACCTGTTGAGTTTGC
                                                                                                                                                                                                                                                               1648 CAAGAAGAAGAAGCGCTCCAAGGCCAAGGCGGAGCGAGGCGTCCCCTGCCGACCTCCC
                                                                                                                                                                                                                                                                                                                685 AATAGATCCTAATGAACCTACATACTGCTTATGCAACCAAGTGTCTTATGGGGAGATGAT
                                                                                                                                                                                                                                                                                                                                                                                                                     745 AGGATGTGACAATGAACAGTGTCCAATTGAATGGTTTCACTTTTCATGTTTCACTTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          805 CTATAAACCAAAGGGGAAATGGTATTGCCCAAAGTGCAGGGGAGATAATGAGAAAACAAT
                                                                                                       565 GGCAAATGGGATTGAAGACTGTGATGATCAGCCACCTAAAGAAAAGAAATCCAAGTCAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: p33/ING1 as a Mediator of p53 Signaling Pathway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff STREET: 300 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5888 GGACAAAGCCCTGGAGAATCCAAAAAAGAGAG 6920
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APPLICATION NUMBER: US/09/006,783A
FILING DATE: 15-JAN-1998
ATTORNEY/AGENT INFORMATION:
NAME: NO. US20030073084Alnan, Kevin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/968,653A
FILING DATE: 01-Oct-2001
CLASSIFICATION: <UNKnown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 97,837
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2, Application US/09968653A Publication No. US20030073084A1 GENERAL INFORMATION:
APPLICANT: Gudkov, Andrey V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
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STRANDEDNESS: single
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Riabowol, Karl
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Drive

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South Wacker
                         STATE: Illinois
            Chicago
                                  COUNTRY: USA
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Best Local Simi
Matches 250;
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                                                                                                                                                                                                                          AGGTGGACAGCCACGTGGAGCTGTTCGAGGCGCAGCAGGAGCTGGGCGACACAGTGGGCA
                                                                                                                                                                                                                                                                                                   -CTGCTGAAAGTGAACGAGCCTCAGATAAAGCAAAGATGGATTCCAGCCAACCAGAAAGA
                                                                                                                                                                                                                                                                                                                        434 ACAGCGGCAAGGTTGGCGCGCGCACAGGCCCAATGGCGATGCGGTAGCGCAGTCTGACAAGC
                                                                                                                                                                                                                                                                                                                                              TCTTCAAGAA; -GACCCCGCAGGCAGCGGACCAGTGAAAGCCGTGATTTATGTCACATGG
                                                                                                                                                                                                                                                                                                                                                                   194 CCAACAGCAAGCGCTCACGGCGGCAGCGCAACAACGAAACGTGAGAACGCGTCCAGCA
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                                                                                                                                                                                                                                                                                                                                                                                                               ACCACGACCACGACGGCGCCTCGGGCACACCCAAGGAGAAGAAGGCCAAGACCTCCA
                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 p53 Signaling
                                                                                                   30;
                                                                            Length 2061;
                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: p33/ING1 as a Mediator of Pathway
                                                                             DB 9;
                                                                                                  0; Mismatches 268;
                                                                           Query Match
Best Local Similarity 56.9%; Pred. No. 3.2e-34.
Matches 393; Conservative 0; Mismatches 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACAAAAGTACTGAAAAGACAAAAAAGGATAG 897
                                                                                                                                                                                                                                                          AAATGGAGTTACACTCACAGTGTTTCCAAGATC-
                    NAME/KEY: CDS
LOCATION: 16.897
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-968-653A-6; Sequence 6, Application US/09968653A; Publication No. US20030073084A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Gudkov, Andrey V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Garkavstev, Igor
Riabowol, Karl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
  CDNA
MOLECULE TYPE:
FEATURE:
                                                     US-09-968-653A-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AATGGTATTGCCCAAAGTGCAGGGGAGATAATGAGAAAACAATGGACAAAAGTACTGAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                522 CCCGCAGCCAGCGGACCAGTGAAAGCCGTGATTTATGTCACATGGCAAATGGGATTGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  242 CACGGCGGCAGCGCAACAACGAGAACGTGAGAACGCGTCCAGCAACCACGACCACGACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CCAAGGCCAAGCAGGAAAGGGAAGCTTCACCTGTTGAGTTTGCAATAGATCCTAATGAAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AGTGCCCCATCGAGTGCTTCCACTTCTCGTGCGTGGGGCTCAATCATAAACCCAAGGGCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 633;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 174.4; DB 9;
Pred. No. 1.2e-32;
); Mismatches 126;
                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: NO. US20030073084Alnan, Kevin
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 97,837
                                                                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/968,653A
FILING DATE: 01-Oct-2001
CLASSIFICATION: <UNKnown>
                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/006,783A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: CDS
LOCATION: 1.630
SEQUENCE DESCRIPTION: SEQ ID NO: US-09-968-653A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 8
US-10-037-270-435
; Sequence 435, Application US/10037270
                                                                                                                                                                                                              FILING DATE: 15-JAN-1998
                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION
                    MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                               FELEPHONE: 312-913-0001
                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 633 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                             TELEFAX: 312-913-0002
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
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66.58;
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COMPUTER READABLE FORM:
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AATCCAAAAAAGAGAG
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169 CGTGGAGTCGCTGCCCCACGACATGCAGAGGAACGTGTCTGTGCTGCGAGAGCTGGACAA 228
                                                                                                                                                                                                                                                                                                                                                                               76 GAAATACCAAGAGATCCTGAAGGAGCTAGACGAGTGCTACGAGGCGCTTCAGTCGCGAGAC 135
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              169 CGTGGAGTCGCTGCCCCACGACATGCAGGAACGTGTCTGTGCTGCGAGAGCTGGACAA 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   349 AGAATTGGGGAGATGAAAAAATACAGATŤGTTACACAAATGCTCGAATTGGTGGAAAATCG
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                                                                                                                                                                                                             Length 451;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TITLE OF INVENTION: THE THERAPY AND DIAGNOSIS OF LUNG CANCER FILE REFERENCE: 210121.475C9
                                                                                                                                                                                                                                                    Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       255 CACGCGGCAGGTGGACAGCCACGTGGAGCTGTTCGAGG 292
                                                                                                                                                                                                           Score 83.6; DB 9;
Pred. No. 1.5e-10;
0; Mismatches 114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 7.7%; Score 83.6; DB 10; Best Local Similarity 58.6%; Pred. No. 1.5e-10; Matches 163; Conservative 0; Mismatches 114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/738,973
CURRENT FILTED DATE: 2000-12-14
NUMBER OF SEQ ID NOS: 587
SOFTWARE: FASTSEQ for Windows Version 3.0
CURRENT APPLICATION NUMBER: US/09/854,133
CURRENT FILING DATE: 2001-05-11
NUMBER OF SEQ ID NOS: 735
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 146, Application US/09738973
Patent No. US20020110563A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Reed, Steven G.
Henderson, Robert A.
Lodes, Michael J.
Fling, Steven P.
Mohamath, Raodoh
                                                                                                                                                                                                             7.78;
58.68;
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APPLICANT: Secrist, Heather
APPLICANT: Indirias, Carol 1
APPLICANT: Benson, Darin R.
APPLICANT: Elliot, Mark
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mannion, Jane
Kalos, Michael D.
                                                                                                                                                                                                             Query Match 7.7
Best Local Similarity 58.6
Matches 163; Conservative
                                                                                                                        ; TYPE: DNA
; ORGANISM: Homo sapien
US-09-854-133-146
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                                                                                    SEQ ID NO 146
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APPLICANT:
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                                                                                                         LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GITTCACTTACCTATAAACCAAAGGGGAAATGGTATTGCCCAAAGTGCAGGGGAGATAAT 853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  674 GTTGAGTTTGCAATAGATCCTAATGAACCTACATACTGCTTATGCAACCAAGTGTCTTAT
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APPLICANT: Lodes, Michael J.
APPLICANT: Mchamath, Racdoh
APPLICANT: Henderson, Robert A.
APPLICANT: Benson, Darin R.
APPLICANT: Secrist, Heather
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
FILLE OF INVENTION: THE THERAPY AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.475C10
                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: No. US20030104529Alel Nucleic Acids and
TITLE OF INVENTION: Polypeptides
FILLE REFERENCE: 744C1P2B
CURRENT APPLICATION NUMBER: US/10/037,270
CURRENT FILING DATE: 2002-01-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 91.6; DB 9; Length 19
Pred. No. 4.1e-12;
0; Mismatches 74; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1394 AAGAGAAGAGCCAGCAGACACAAATAAAGG 1423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 854 GAGAAAACAATGGACAAAAGTACTGAAAAG 883
                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR FILING DATE: 2002-01-04

PRIOR APPLICATION NUMBER: 09/52,317

PRIOR FILING DATE: 2000-04-25

PRIOR PELICATION NUMBER: 09/488,725

PRIOR FILING DATE: 2000-01-21

NUMBER OF SEQ ID NOS: 1104

SOFTWARE: pt_Ft_genes Version 1.0

TENGEN: 100
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Publication No. US20020183499A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8.5%;
64.8%;
No. US20030104529A1
                                                                                                                                                                                                                                                                                                                                                         Tillinghast, John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 8.55
Best Local Similarity 64.87
Matches 136; Conservative
                                                                                                                                                                                                                            Yang, Yonghong
Wang, Jian-Rui
Zhou, Ping
                                                                                                                                                                 Zhao, Qing A.
Wehrman, Tom
Xue, Aidong J.
                                                                                                                      Ren, Feiyan
Chen, Rui-hong
                                         APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenghua
APPLICANT: Asundi, Vinod
APPLICANT: Zhang, Jie
                                                                                                                                                                                                                                                                                      Ma, Yunqing
Wang, Dunrui
Wang, Zhiwei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: CDS
LOCATION: (164)..(1420)
US-10-037-270-435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-854-133-146
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APPLICANT:
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APPLICANT: NIED. VOCA
APPLICANT: NIED. VOCA
APPLICANT: NIED. VOCA
APPLICANT: NIED. VOCA
APPLICANT: ALM, TONG
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
TITLE OF INVENTION: SAME, AND METHODS OF USE
FILE REFERENCE: SCRIP1300-3
CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT FILING DATE: 2001-08-24
PRIOR FILING DATE: 2001-08-24
PRIOR FILING DATE: 2001-08-14
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-01-16
PRIOR PLING DATE: 2001-01-16
PRIOR STELING DATE: 2001-01-16
PRIOR STELING DATE: 2001-01-16
PRIOR PLING DATE: 2001-05-20
PRIOR PLING DATE: 2001-01-16
PRIOR PLING DATE: 2001-01-16
PRIOR PLING DATE: 2001-01-16
PRIOR PLING DATE: 2001-01-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 729 CITATGGGGAGATGATAGGATGTGACAATGAACAGTGTC---CAATTGAATGGTTTCACT 785
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             661
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7 GNCCCCATTGTCGNACCCCTAGTCCGTGTGGTGGAATTCGGCGACCGCCATGTACTTGGA 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               602 CCTTTGGAGACATGATTGCCTGTGACAATGAGAATTGCCAAGGAGGTGAATGGTTTCACT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              786 TITCATGITITCACTIACCIAIAAACCAAAGGGGAAAIGGIAIIG 831
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          662 ATACATGCGTTGGCCTCACACCTGAGACCAGATTCAAAGGGAAATG 707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 813;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
TITLE OF INVENTION: FROW VARIOUS CDNA LIBRARIES
FILE REFERENCE: 20411-756
CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT FILING DATE: 2001-07-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 5.3%; Score 56.8; DB 9; Best Local Similarity 49.4%; Pred. No. 0.00053; Matches 179; Conservative 0; Mismatches 174;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4.1e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 62; DB 9;
Pred. No. 4.1e-0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
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PRIOR FILING DATE: 1999-01-20
NUMBER OF SEQ ID NOS: 38054
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 16047, Application US/09918995
Publication No. US20030073623A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc_feature
LOCATION: (1)...(456)
OTHER INFORMATION: n = A,T,C or G
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Arabidopsis thaliana US-09-938-842A-1178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5.7%;
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Matches 108; Conservative
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TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production in Fungi
FILE REFERENCE: 109272.147
76 GAAATACCAAGAGATCCTGAAGGAGCTACACGAGTGCTACGAGCGCTTCAGTCGCGAGAC 135
                                                                                                                          698 GAACCTACATACTGCTTATGCAACCAAGTGTCTTATGGGGAGATGATAGGATGTGACAAT 757
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                                                                                             289 IGATITAAACCAGAAGAAACGICTACAGCAGCTTCTCCAGAGAGCACTAATTAATAGTCA
                                                                                                                                                                                          349 AGAATTGGGAGATGAAAAAATACAGATTGTTACACAAAATGCTCGAATTGGTGGAAAATCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    758 GAACAGTGTCCAATTGAATGGTTTCACTTTTCATGTGTTTCACTTACCTATAAACCAAAG
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                                                                                                                                                                                                                                                                                                                            255 cacecedeaegregacaeccaceregaecrerreage 292
                                                                                                                                                                                                                                                                                     409 GGCAAGACAAATGGAGTTACACTCACAGTGTTTCCAAG 446
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Pred. No. 3.5e-06;
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PRIOR APPLICATION NUMBER: US 09/487,558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION
PRIOR FILING DATE: 2000-01-19
PRIOR APPLICATION NUMBER: US 60/160,587
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; Sequence 1178, Application US/09938842A
; Patent No. US20020160378A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 257, Application US/09801368
Patent No. US20020128250A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn version 3.0
SEQ ID NO 257
LENGTH: 993
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ilarity 66.2%;
Conservative
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APPLICANT: Busby, Robert
APPLICANT: Cali, Brian
APPLICANT: Hocht, Peter
APPLICANT: Holtzman, Doug
APPLICANT: Madden, Ketin
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Salama, Sofie
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NUMBER OF SEQ ID NOS: 440
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Best Local Similarity
Matches 96; Conserv
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385 AATGCTCGAATTGGTGGAAAATCGGGCAAGACAAATGGAGTTACACTCACAGTGTTTCCA 444
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                                                                                          127 GCGAGAGCTGGACCAGAGGACGGAAGATAAGAAAGCAGAGATTGACATCCTGGCTGCAGA 186
                                                                                                                                274 ATATAA-----GAAAGAAGATGATTTAAACCAGAAGAAGGTCTACAGCAGCTTCT 324
                                                                                                                                                                                                         CCAGAGAGCACTAATTAATAGTCAAGAATTGGGAGATGAAAAAATACAGATTGTTACACA 384
                                                                                                                                                                                                                                                                                                                   307 GACCTACGAGATGGTGGATAAACACATTCGAAGGCTTGATGCAGACCTGGCGCGCGTTTGA 366
                                                                                                                                                                   187 GTACATCTCCACGGTGAAGACGCTGTCTCCAGACCAGCGCGTGGAGCGCCTGCAGAAGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                847 AGATAATGAGAAAACAATGGACAAAAGTACTGAAAAAGACAAAAAAGGATAGAAGATCGAG
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Pred. No. 0.0089;
0; Mismatches 114; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ) ORGANISM: Bos taurus
) OTHER INFORMATION: Clone ID: 20-LIB3057-013-Q1-K1-E7
US-09-960-352-4582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Warren, Wesley C.
APPLICANT: Tao, Nengbing
APPLICANT: Byatt, John C.
APPLICANT: Byatt, John C.
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECU
TITLE OF INVENTION: MUSCLE AND EAT DEPOSITION
TITLE OF INVENTION: MUSCLE AND EAT DEPOSITION
FILE REFERENCE: 16511.006/37-21(10298)C
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
SEQ ID NOS: 15112
LENGHH: 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 4582, Application US/09960352 Patent No. US20020137139A1 GENERAL INFORMATION:
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Best Local Similarity 51.3%;
Matches 120; Conservative
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AG 368
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APPLICANT: Pyle, Ruth

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### APPLICANT: Xu, Jiangchun

### APPLICANT: Secrist, Heather

### TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

### TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

### TITLE OF INVENTION: COMPOSITIONS OF COLON CANCER

### FILE REPRENCE: 210121.552

### CURRENT APPLICATION UNDER: US/09/919,580

### SECTION NOT 14

### CONTINUED NO 114

### CONTINUED NO 115

### CONTINUED NO 115
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Search completed: June 20, 2003, 02:45:35 Job time: 195 secs

680.8 63.0 919 12 BG211544 671.8 62.2 675 14 BM682789 663 61.4 664 14 BM719460 636.4 58.9 653 13 B1091047 607 56.2 708 13 B1495873 553.4 52.2 574 10 AV647917 554.2 51.3 564 12 BB839427 550.8 51.0 703 13 B1546850	547 50.6 547 9 AII86701 538.2 49.8 566 12 BE839460 528 49.8 541 12 BF114684 528 48.9 552 9 AI800614 521 48.2 537 9 AI458721 513 47.5 513 9 AI458721 513 47.5 525 9 AI885642 508.4 47.1 601 14 BQ206861 496.2 45.9 522 13 BI495874	27 480.2 44.5 502 12 BF732679 28 477 44.2 477 12 BF511151 29 469.2 43.4 720 12 BE831862 30 468.6 43.4 720 9 AA797495 31 466.4 43.2 830 12 BG189892 32 462.8 42.9 466 9 AI818729 33 455 42.1 455 10 AM052211 34 454 42.0 555 14 BO133330	C 35 452.8 41.9 466 9 AI126389 AZ24672 AAZ268672 AAZ268672 AAZ268672 AAZ2687672 AAZ2687672 AAZ2687672 AAZ2687676 AZ2687676 AZ268767777 AZ268787877 AZ268777 AZ268777 AZ268777 AZ268777 AZ268777 AZ26877 AZ2687 AZ26877 AZ2687 A	ALIGNMENTS	•	ORGANISM Mus musculus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Murinae; Mus. REFERENCE 1 AUTHORS Carninci,P. and Hayashizaki,Y. TITLE High-efficiency füll-length cDNA cloning JOURNAL Meth. Enzymol. 303, 19-44 (1999) PUBMED 10349636	
GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd. OM nucleic - nucleic search, using sw model Run on: June 20, 2003, 01:20:25; search time 1533 Seconds (without alignments) 14409.736 Million cell updates/sec	ct score: US-09-513-365A-2 ct score: 1080 nce: 1 gcggccgcggtgcatgaaaaaaaaaaaaaaaaa ng table: IDENTITY_NUC Gapop 10.0 , Gapext 1.0 hed: 16154066 seqs, 8097743376 residues	Total number of hits satisfying chosen parameters: 32308132 Minimum DB seq length: 0 Maximum DB seq length: 2000000000 Post-processing: Minimum Match 100% Listing first 45 summaries	īn	11: gb_htc:* 12: gb_est3:* 13: gb_est4:* 14: gb_est5:*	15: em_estfun:* 16: em_eston:* 17: 9b_gss.* 18: em_gss_hum:* 20: em_gss_ln:* 21: em_gss_vrt:* 22: em_gss_vrt:* 23: em_gss_nus:* 24: em_gss_nus:* 25: em_gss_nus:* 26: em_gss_pro:*	Pred. No. is the number of score greater than or equal and is derived by analysis	No. Score Match Length DB ID 1 812.8 75.3 1464 11 AKO12716 2 747.8 69.2 912 14 BQ277444 c 3 735 68.1 735 14 BM982877 c 4 727.6 67.4 798 12 BG184056 5 711 65.8 778 13 BI548536 6 694.2 64.3 778 13 BI548536 BEST96780 BI548536 603191255

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with XhoI and SstI. Cloning sites,
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                                                                                                           Location/Qualifiers
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Best Local Similarity 88.0
Matches 932; Conservative
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1464
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Arakawa.T., Baldarelli,R., Bono,H., Brownstein,M., Bult.C.,
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Sogabe,Y., Sulto,R., Shibata,Y., Shinagawa,A., Takahashi,F.,
Tanaka,T., Tejima,Y., Toya,T., Yamamura,T., Yamanaka,I.,
Yasunishi,A., Yoshida,K., Yoshino,M., Muramatsu,M. and
                    Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikagami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system-1384-format Genome Res. 10 (11), 1757-1771 (2000)
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Pred. No. 2.7e-114;
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National Institutes of Health, Mammalian Gene Collection (MGC)
L Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs r@mail.nih.gov
Tissue Procurement: NCI
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCALQ08 row: h column: 10
High quality, sequence stop: 587.
Location/Qualifiers
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LICEL CLOSS ROW: LLDL CLOSS ROW: 
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 912)
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/clone_llb="NHH_MGC_127"
/tisbue_type="mixed (pool of 40 RNAs)"
/lab_host="BH108 (T1-phage-resistant)"
/note="Vector: pDNR-LIB; Site_l: Sfil (ggccattatggcc);
                                                                                                                                                                                                                                                                          ACCAGTGAAAGCCGTGATTTATGTCACATGGCAAATGGGATTGAAGACTGTGATGATCAG
                        CCACCTAAAGAAAAGAAATCCAAGTCAGCAAAGAAAAAGAAACGCTCCAAGGCCAAGGAG
                                                                                                       GAAAGGGAAGCITCACCIGITGAGITTGCAATAGATCCTAATGAACCTACATACTGCITA
                                                                                                                                                                                                                                                  TGCAACCAAGTGTCTTATGGGGAGATGATAGGATGTGACAATGAACAGTGTCCAATTGAA
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Pred. No. 2.5e-104;
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                                                                                                                                                                                                                                                                                                                                                             Total Total Lowa Med Labs, Iowa City, IA 52242, USA Tel: 319 356 4866
Fax: 319 356 4866
Fax: 319 356 7171
Famil: paul-mccray@uiowa.edu
Tissue Procurement: Dr. M. J. Welsh, University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com).
Seq primer: M13 FORWARD
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TAG_TISSUE-Human Lung Epithelial Cell Lines untreated LPS
6hr to LPS 24h
720 CCAATTGAATGGGTTCACTTTTTCATGTGGTTCACTTACCTATAAACCCAAAGGGGAAAT 779
                                                                                                                                                                                                              Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 735)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
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                                        GGTATTGCCCAAAGTGCAGGGGAGATAATGAGAAAACAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone="UI-CF-EN1-acs-d-05-0-UI"
/clone_lib="UI-CF-EN1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                            Genome Res. 6 (9), 791-806 (1996)
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BM982877.1 GI:19606826
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100.0%;
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Contact: McCray, PB
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Best Local Similarity
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Length 735;

Score 735; DB 14; Pred. No. 2.4e-102;

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Eukaryotta, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases I to 78)
Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R.,
Cain,S., Leventhal,C., Thornton,M., Ramachandran,R., Whittington,J.,
Lerner,L., Costanzo,D., McElligott,K., Boozer,S., Mays,R., Smith,E., Velcso,N., Klika,A., Hess,J., Cothren,K., Lo,K., Offenbacher,C., Danzig,J. and Ducarry.
Creation of genome-wide protein expression libraries using random
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RST2972 Athersys RAGE Library Homo sapiens CDNA, mRNA sequence.
BG184056 BG184056.1 GI:13705743
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GGGTAAATGCATAAGACTATGCAATAATTTTTAATCATTAGTATTAATGGTGTGTATTAAAA 1040
                                                                                                                                                                                                                                                   BE796780 793 bp mRNA linear EST 20-SEP-2000 601587557F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3941655 5',
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                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 793)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCA794 row: a column: 16
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National Institutes of Health, Mammallan Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
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Pred. No. 1e-98;
); Mismatches
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="TRAGE:3941655"
/clone=lib="NIH_MGC_7"
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                                                                                                                                                                                                                            /clone_lib="Athersys RAGE Library"
/cell_line="HT1080"
/note="See 'Creation of Genome-wide Protein Expression
Libraries using Random Activation of Gene Expression,
Nature Biotechnology, in press. Note that even though the
cell type indicated is HT1080, since a random activation
method was used, these sequence tags are not necessarily
expressed in HT1080 under normal circumstances."
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                                                              Athersys, Inc.
3201 Carnegie Ave, Cleveland, OH 44115, USA
Tel: 216 431 9900
Fax: 216 361 9596
Email: scain@athersys.com
                                                                                                                                                                                                                                                                                                                                                                                                                     DB 12;
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Pred. No. 3.1e-101;
0; Mismatches 4;
                 440-445 (2001)
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/db_xref="taxon:9606"
                                                                                                                                                High quality sequence stop: 531.
Location/Qualifiers
   expression
               Nat. Biotechnoľ. 19 (5),
21227151
                                                 Contact: Scott J. Cain
                                                                                                                                                                                                                                                                                                                                                                                                                 67.4%;
   gene
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Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
Toshiyuki and Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAMI1661 row: n column: 13
High quality sequence stop: 775.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                      778 bp mRNA linear EST 05-SEP-2001 603191255F1 NIH_MGC_95 Homo sapiens cDNA clone IMAGE:5262540 5', B1548536 B1548536.1 G1:15435848
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NIH-WGC http://mgc.nci.nih.gov/.
                  TGAAAAAATACAGATTGTTACACAAATGCTCGAATTGGTGGAAAATCGGGCAAGACAAAT
                                                                                                                                                  CTAAAGAAAAGGAAATCCAAGTCAGCAAAGAAAAAGAAACGCTCCAAGGCCAAGCAGGAAA
                                                           GAAGAAACGICTACAGCAGCITCICCAGAGGACCTAATTAATAGICAAGAATTGGGAGA
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                                                                                                                                                                       DB 13; Length 778;
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Best Local Similarity
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TCGTTTGCTTTCAGAAAATGTTTTAGGGTAAATGCATAAGACTATGCAATAATTTTTAAT 1015
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Tissue Procurement: Dr. Gregg Hageman
CDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa
DNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa
Clone Distribution: Researchers may obtain clones from Research
                                                                                                                                                                                                                                                                                                                                                                                       Euteleostomi;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 675)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
                   /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="Ul-12J1-ajf-g-22-0-Ul"
/clone="Lib="UI-E-E11"
/tissue_type="fetal eyes, lens, eye anterior segment,
                                                                         656 GAAAGGGAAGCTTCACCTGTTGAGTTTGCAATAGATCCTAATGAACCTACATACTGCTTA
                                                                                                                                                 716 TGCAACCAAGTGTCTTATGGGGAGATGATAGGATGTGACAATGAACAGTGTCCAATTGAA
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                                                                                                                                                                                                                                                                                                                                   601 NAGTGCAGGGGAGAATATGAGAAAACAAAG--ACAAAGCACTGAAAAGACAAAAAGG-T
AGAAGATCGAGGTAGTAAAGGCCATCCACATTTTAAAAGGGTTATTTGTCTTTTATATAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
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Seq primer: M13 Forward
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BM682789.1 GI:18992685
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                                                                       BG211544 919 bp mRNA linear EST 21-APR-2001
RST31111 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.
                                                                                                                                                                                                 Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalla, Butheria, Primates; Catarrhini, Hominidae, Homo.

[ (bases 1 to 919)

Harrington, J.J., Sherf, B., Rundlett, S., Jackson, P.D., Perry, R., Cain, S., Leventhal, C., Thornton, M., Ramachandran, R., Whithington, J., Lerner, L., Costanzo, D., McBlilgott, K., Boozer, S., Mays, R., Smith, E., Veloso, N., Klika, A., Hess, J., Cothren, K., Lo, K., Offenbacher, J., Dazigh, J. and Ducar, M.

J. Dazigh, J. and Ducar, M.

Zeration of gene expression libraries using random activation of gene expression.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CAAATGGAGTTACACTCACAGTGTTTCCAAGATCCTGCTGAAAGTGAACGAGCCTCAGAT
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Pred. No. 3.5e-94;
0; Mismatches 30; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                            Athersys, Inc.
3201 carnegie Ave, Cleveland, OH 44115, USA
TTE1: 216 431|9900
Fax: 216 361|9596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db/xref-"taxon:9606"
/clone_lib="Athersys RAGE Library"
/cejl_line="HT1080"
                                                                                                                                                                                                                                                                                                                                                                            Nat. Biotechnol. 19 (5), 440-445 (2001)
21227151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
                                                                     919 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       High quality sequence stop: 439.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: scain@athersys.com
                                                                                                                           BG211544.1 GI:13733231
                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Scott J. Cain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63.0%;
95.1%;
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75 TATGCAATAATTTTTAATCATTAGTATTAATGGTGTATTAAAAGTTGTTGTACTTTGAAA 16
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/db_xref="taxon:9606"
/clone="UT-E-EJ1-ajf-g-22-0-UI"
/clone_lib="UI-E-EJ1"
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97044477
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                     /Gev stage="fetal and adult"
//lab_host="DH10B (Life Technologies) (TI phage resistant)".
//lab_host="DH10B (Life Technologies) (TI phage resistant)".
//note="Organ: eye; Vector: pyT73-pac (Pharmacia) with a modified polylinker; Site_1: ECOR I; Site_2: Not I; UI-E-EJI is a subtracted CDNA library constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-df primer containing a Not I site. Double stranded cDNA was ligated to an ECOR I adaptor, digested with Not I, and cloned directionally into pyT73-pac vector. The oligonoucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tall. The sequence tags for this library are: fetal eyes, AGNATCAGGA; lens, CGATTAGCGS, retina, CGCGCAT; optic nerve, CCATTAAGGS; retina, CCGCS, Retina Foveal and Macular, GTCC; RPE and Chorold, ACCTA. This library was created for the program, Gene Discovery in the Visual mach retire.
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99.7%;
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according to Bonaldo. Lennon and Soares, Genome Research, 6:791-806, 1996. First strand CDNA synthesis was primed with an oligo-dr primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT773-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tags for this library are: fetal eyes, AGANCCAAGA; eye anterior segment, AATGCCGCAT; optic nerve, CCATTAAGTG; retina, CGCGG; Retina Foveal and Macular, GTCC; RPE and Choroid, ACCTA. This library was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute (NEI)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 358 9565
Email: msoares@blue.weeg.ulowa.edu
Tissue Procurement: Dr. Gregg Hageman
CDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com).
Seq primer: M13 Reverse.
                                                        EST 01-MAR-2002
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//dev_stage="fetal and adult"
//lab_host="DH10B (Life Technologies) (T1 phage resistant)"
//note="Corgan: eye; Vector: pT713-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not I; U1-E-EJ1 is a subtracted cDNA library constructed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue_type="fetal eyes, lens, eye anterior segment, optic nerve, retina, Retina Foveal and Macular, RPE and
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664 bp mRNA linear EST 01-UI-E-EJ1-ajf-g-22-0-UI.rl UI-E-EJ1 Homo sapiens cDNA clone UI-E-EJ1-ajf-g-22-0-UI 5', mRNA sequence.
BM719460
EST.
                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteļe
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 664)
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75 Francis Street,
Tel: 617 732 7980
Fax: 617 738 6996
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Robertson, N.G., Khetarpal, U., Gutlerrez-Espeleta, G.A., Bleber, F.R., and Morton, C.C.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 653)
          GTTACACAAATGCTCGAATTGGTGGAAAATCGGGCAAGACAAATGGAGTTACACTCACAG
                    CAACCAGAAAGATCTTCAAGAAGACCCGCAGGCAGCGGACCAGTGAAAGCCGTGATTA
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                                                                  TGTCACATGGCAAATGGGATTGAAGACTGTGATGATCAGCCACCTAAAGAAAAGAAATCC
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B1495873 | S11532577-
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Departments of Pathology and
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                                                       Institutes
                                     Email: ccmorton@bics.bwh.harvard.edu
DNA sequencing and analyses were performed by National Institut
of Health Intramural Sequencing Center (NISC; see
http://www.nisc.nih.gov).
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information
Plate: LLAM6327 row, G column: 7
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 Harvard Medical School, Boston, MA
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Pred. No. 2.3e-87;
); Mismatches 1; ]
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99.8%;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo. Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 708)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)

L Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: Ggapbs-rémail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki Toshiyuki and Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BI460319 708 bp mRNA 11near EST 21-AUG-2001 603201967F1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:5267729 5',
                                                                                                                                                                                                                                   873 GTACTGAAAAGACAAAAAAGGATAGAAGATCGAGGTAGTAAAAGGCCATCCACATTTTAAA 932
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753 ACAATGAACAGTGTCCAATTGAATGGTTTCACTTTTCATGTGTTTCACTTACCTATAAAC
                                                                                                                                                      813 CAAAGGGGAAATGGTATTGCCCAAAGTGCAGGGGAGATAATGAGAAAAACAATGGACAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                            http://image.lnl.gov
Plate: LLAM11675 row: f column: 18
High quality sequence stop: 700.
Location/Qualifiers
1. 706
/organism="Homo sapiens"
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/clone="IMAGE:5267729"
/clone_lib="NIH_MGC_97"
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BI460319
BI460319.1 GI:15250975
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                                                                                                                                                BI091047 891 bp mRNA linear EST 20-JUN-2001 602855235F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:4996593 5', mRNA sequence.
BI091047.1 GI:14509377
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ITGGTGGAAAATCGGGCAAGACAAATGGAGTTACACTCACAGTGTTTCCAAGATCCTG-C 453
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                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I (bases 1 to 801)
NHF-NGC http://mgc.nol.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: ATCC
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CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Incyte Genomics, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LiAMIIO22 row: column: 10
High quality sequence stop: 722.
Location/Qualifiers
1. 891
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                    DB 13;
                                  58.5%; Score 632.2; DB 1
96.5%; Pred. No. 8.2e-87;
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/db_xref="taxon:9606"
/clone="IMAGE:4996593"
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/cell_line="MGC36"
/lab_host="DH108"
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/Organism="Homo sapiens"
/db_aref="taxon:9606"
/db_aref="dcBbD03"
/clone="GLCBbD03"
/clone=Ltype="corresponding non cancerous liver tissue"
/dev_stage="Adult"
/lab_host="SolR"
/note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2
              Pudong, Shanghai
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Chinese National Human Genome Center at Shanghai 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, 120103, Pr. R. China Tel: 86-21-50801919(ex.45)
Fax: 86-21-50801922
Email: hansg@edgc.sh.cn
This clone is available at CHGC in Shanghai.
Location/Qualifiers
                                                                                                                                                                                                                                                    Score 599; DB 10;
Pred. No. 1e-81;
; Mismatches 22;
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

La (bases 1 to 679)

Xu,X., Huang,J., Xu,Z., Qian,B., Zhu,Z., Yan,Q., Cai,T., Zhang,X.,
Xiao,H., Qu,J., Liu,F., Huang,Q., Cheng,Z., Li,N., Du,J., Hu,W.,
Shen,K., Lu,G., Fu,G., Zhong,M., Xu,S., Gu,W., Huang,W., Zhao,X.,
Hu,G., Gu,J., Chen,Z. and Han,Z.
Insight into hepatocellular carcinogenesis at transcriptome level
by comparing gene expression profiles of hepatocellular carcinoma
with those of corresponding noncancerous liver

L proc: Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)

E 2165106

Contact: Zeguang Han
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                          Length 708;
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                        Score 607; DB 13;
Pred. No. 6.1e-83;
); Mismatches 6;
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National Institutes of Health, Mammalian Gene Collection (MGC)

National Institutes of Health, Mammalian Gene Collection (MGC)

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Other_ESTS: ba59f06.y1

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-rémail.nh.gov

Tissue Procurement: ATC

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

image.llnl.gov/image/html/iresources.shtml

Seq primer: -40UP from Gibco

High quality sequence stop: 420.

Location/Qualifiers

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                                                                                           Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Organ: cervix; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dr. Average insert size 1.5 kb. Library prepared by Life Technologies."
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DaS9f06.xl NIH_MGC_10 Homo sapiens cDNA clone IMAGE:2900867 3' similar to TR:095698 095698 ING1LP. ;, mRNA sequence. AW674008
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Pred. No. 2.8e-76;
0; Mismatches 7; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/db_xref="taxon:9606"
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/clone_lib="NIH_MGC_10"
/cell_line="MGC36"
/lab_host="DH108"
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This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl-&t2-RC3-FN0143-190 Seq primer: puc 18 forward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Organ: prostate_normal; Vector: puc18; Site_1: Smal Site_2: Smal; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent Products dorived from ORESTES PCR (U.S. Letters Patent Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions.
                                                                                                                                                                                                                                                                                                                                                               EST 22-SEP-2000 mRNA sequence.
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Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
,M.J., Sagres,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                           AGAAAATGTTTTAGGGTAAATGCATAAGACTATGCAATAATTTTTAATCATTAGTATTAA 1027
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                                                                                                     94 AGAAAATGTTTAGGGTAAATGCATAAGACTATGCAATAATTTTTAATCATTAGTATTAA 35
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Simpson A.J.G.
Laboratory of Cancer Genetics .
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Shotgun sequencing of the human transcriptome with ORF expressed
Gaps
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BE839427 GI:10271805
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                                                                                                                                                                                                           0; Mismatches
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TCGTCGGCTGCGCTGACCGGGGGGGGGGCGGCTGCTCACCTGCTACGTGCAGGAC 157 	TACCTTGAGTGCGTGGAGTCGCTGCCCCACGACATGCAGGAACGTGTCTGTGCTGCGA 217 	GAGCTGGACAACAAATATCAAGAAACGTTAAAGGAAATTGATGATGTCTACGAAAAATAT 277 11111111111111111111111111111111111	AAGAAAGAAGATTTAAACCAGAAGAAACTCTACAGCAGCTTCTCCAGAGAGCACTA 337 	attaatagtcaagaattgggagatgaaaaaatacagattgttacacaaatgctcgaattg 397 	GTGGAAAATCGGGCAAGACAAATGGAGTTACACTCACAGTGTTTCCAAGATCCTGCTGAA 457 	AGTGAACGAGCTCAGATAAAGCAAAGATGGATTCCAGCCAACCAGAAGATGTTCAAGA 517 	agacccccadgecagcgaccagtgaaagccgtgatttatgtcacatgccaaatgggatt 577 	GAAGACTGTGATGATCAGC 596
TCGTCGGC	TACCTTGA TACCTTGA	GAGCTGGA GAGCTGGA	AAGAAAGA AAGAAAGA	ATTAATAC 	GTGGAAAA 	AGTGAACG 	AGACCCCG 	GAAGACTG
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anchorage dependence; apoptosis; tumour; cancer; gene therapy; ds.
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/product= "Tumour suppressor homologue protein, p33ING2"
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Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                              The present sequence is a DNA encoding tumour suppressor homologue protein, p331NG2 which is homologous to human tumour suppressor protein, p471NG3. The tumour suppressors of the invention are involved in the regulation of cell proliferation and in the control of cellular aging, anchorage dependence and apoptosis. The tumour suppressor protein, p471NG3, nucleic acids encoding it and antibodies against it are useful for diagnosis, prevention and treatment of tumours and cancers. The p471NG3 DNA is also used in gene therapy.
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100.0%; Pred. No. 1.5e-236;
tive 0; Mismatches 0;
                                                 Disclosure; Page 78; 80pp; English
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Matches 1080; Conservative (
2001-488975/53
      P-PSDB; AAE06675
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                                                                                                                                                        721 CCAAGTGTCTTATGGGGAGATGATAGGATGTGACAATGAACAGTGTCCAATTGAATGGTT
                                          TCACTTTTCATGTGTTTCACTTACCTATAAACCAAAGGGGAAATGGTATTGCCCAAAGTG
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cancer such as cancer of the colon, stomach, oesophagus or fallopian tube, and the screening of candidate drugs for the treatment of such
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); Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human lung-specific gene TSC430 overexpressed in for treatment of, e.g. colon tumour
codon given"
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98JP-0038133.
98JP-0073234.
                                                                                                                                                  AAZ08595 standard; cDNA; 840
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ilarity 99.9%;
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03-FEB-1998;
05-MAR-1998;
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                                                       GACATGCAGAGGAACGTGTCTGTGCTGCGAGAGCTGGACAACAATATCAAGAAACGTTA
                                                                                                                                 CGTCTACAGCAGCTTCTCCCAGAGAGCACTAATTAATAGTCAAGAATTGGGAGATGAAAAA
                                                                                                                                                                     ATACAGATTGTTACACAAATGCTCGAATTGGTGGAAAATCGGGCAAGACAAATGGAGTTA
                                                                                                                                                                                                          CACTCACAGTGTTTCCAAGATCCTGCTGAAAGTGAACGAGCCTCAGATAAAGCAAAGATG
                                                                                                                                                                                                                                                        CGTGATTTATGTCACATGGCAAATGGGATTGAAGACTGTGATGATCAGCCACCTAAAGAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                suppressor (TUSUP) nucleotide sequence,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
277..999
/*tag= a
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TUSUP sequence was identified from a human lung cDNA library. The protein is 240 amino acids in length and has one potential CAMP and CGMP dependent protein kinase phosphorylation site, nine potential protein kinase c phosphorylation site, five potential casein kinase phosphorylation sites, five potential casein kinase phosphorylation sites, five potential casein kinase phosphorylation sites, five potential tyrosine kinase phosphorylation sites, and one potential tyrosine kinase phosphorylation site. TUSUP pass structural and chemical similarity to p33. TUSUP can be used to treat or prevent cancer, particularly of the reproductive or gastrointestinal tracts or of the immune system. Agonists of the TUSUP protein can be used to raise TUSUP specific antibodies and to screen for specific binding agents and potential therapeutic agents. The TUSUP nucleotide sequence can be used in gene therapy and as a source of diagnostic probes and primers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       270
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          511 TTCAAGAAGCCCCGCAGGCAGCGGACCAGTGAAAGCCGTGATTTATGTCACATGGCAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                     This sequence encodes the human tumour suppressor (TUSUP) protein.
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                                                                                                                                                                                                                                                                                                   New human tumour suppressor protein for treating cancer, Freproductive and gastrointestinal tracts or immune system
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1153 BP; 367 A; 215 C; 285 G; 265 T; 21 other;
                 suppressor protein"
                                                                                                                                                                                                                  Patterson C;
/product= TUSUP
/note= "Tumour :
                                                                                                                                                                                                                                                                                                                                                  Claim 7; Fig 1; 71pp; English.
                                                                                                                                                  98US-0086359
                                                                                                               99WO-US11136
                                                                                                                                                                                   (INCY-) INCYTE PHARM INC
                                                                                                                                                                                                                  Corley NC,
                                                                                                                                                                                                                                                  WPI; 2000-062711/05.
P-PSDB; AAY52199.
                                                  WO9961612-A1
                                                                                                                 20-MAY-1999;
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AA247474/c
ID AAZ47474 standard;
                                                                                                        Similarity
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                                                                                                       Best Local Sim:
Matches 343;
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                                                                                                                                 AAGTACTGAAAAGACAAAAAGGATAGAAGATCGAGGTAGTAAAGGCCATCCACATTTA 930
                                                                                                                                                                                                                                                                                                                                                                                           sequence tag; secreted protein; cDNA isolation; mapping; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence is one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. No ORF has yet been conclusively identified within the present sequence. The 5' ESTs were prepared from total human RNAs or|polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because, they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences
                           TGACAATGAACAGTGTCCAATTGAATGGTTTCACTTTTCATGTGTTTCACTTACATAA
                                                                ACCAAAGGGGAAATGGTATTGCCCAAAGTGCAGGGGAGATAATGAGAAAACAATGGACAA
                                                                                                     AAGGGTTATTTGTCTTTTATATATTCGTTTGCTTTCAGAAAATGTTTTAGGGTAAATGC
                                                                                                                                                                                                          ATAAGACTATGCAATAATTTTTAATCATTAGTATTAATGGTGTATTAAAAGTTGTTGTAC
                 TCCTAATGAACCTACATACTGCTTATGCAACCAAGTGTCTTATGGGGAGATGATAGGATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures
                                                                                                                                                                                                                                                                                                                                                                        protein 5' EST, SEQ ID NO: 32534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Giordano J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; SEQ ID 32534; 71pp + CD-ROM; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Duclert A,
                                                                                                                                                                                                                                                                                                                                                                                                     gene therapy; chromosome mapping;
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                                                                                                                                                                                                                                                          TTTGAAAAAAAA 1064
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derived from the 5' ends of mRNAs and even in those cases where longer both sequences have been obtained, the full 5' UTR is rarely included. 5' ESTS are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design expression and secretion vectors.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CAGCAGCTTCTCCAGAGAGCACTAATTAATAGTCAAGAATTGGGAGATGAAAAAATACAG
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                                                                                                                                                                                                                                                                                                                                                                   ATTGTTACACAAATGCTCGAATTGGTGGAAAATCGGGCAAGACAAATGGAGTTACACTCA
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                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   suppressor protein; TUSUP; human; cancer; treat; prevent;
                                                                                                                                                                                                                                                                                        ij
                                                                                                                                                                                                                                         346;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         reproductive tract; gastrointestinal tract; immune system; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human tumour suppressor (TUSUP) fragment nucleotide sequence.
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                                                                                                                                                                                          Sequence 346 BP; 130 A; 63 C; 80 G; 70 T; 3 other;
                                                                                                                                                                                                                                         Score 332.2; DB 2
Pred. No. 3.2e-66;
                                                                                                                                                                                                                                                                                        1; Mismatches
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970 AAAATGTTTTAGGGTAAATGCATAAGACTATGCAATAATTTTTAATCATTAGTATTAATG 1029
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            suppressor protein (TUSDP) see AAY52199. The TUSUP protein is 240 amino acids in length and has one potential CAMP and CGMP dependent protein kinase phosphorylation site, nine potential protein kinase phosphorylation site, five potential casein kinase phosphorylation site, five potential casein kinase phosphorylation site, site, and one potential tyrosine kinase phosphorylation site. TUSUP has structural and chemical similarity to pil TUSUP can be used to treat or prevent cancer, particularly of the reproductive or gastrointestinal used to raise TUSUP specific antibodies and to screen for specific binding agents and potential therapeutic agents. The TUSUP nucleotide sequence can be used in gene therapy and as a source of diagnostic probes
                                                                                                                                                                                                                                                                                                                                                                                                                  849
                                                                                                                                                                                                                                                                                                                                                                 265 AIGTGTTTCACTTACCTATAAACCAAAGGGGAAATGGTATTGCCCCAAAGTGCAGGGGAGA 206
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 sequence was used to determine the sequence of the human tumour
                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                          30.1%; Score 325; DB 21; Length 325; 100.0%; Pred. No. 1.4e-64; Ive 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                          Sequence 325 BP; 103 A; 71 C; 36 G; 115 T; 0 other;
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/product= P37ING1 polypeptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAA53790 standard; cDNA; 2817 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Murine P37ING1 coding sequence.
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/*tag= a
                                                                                                                                                                                                                                                                                                            325; Conservative
                                                                                                                                                                                                                                                                                            Similarity
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1039 ACCCAGAAGCGCCGGGTACTGCACTGCATCCAGAGGCCCTGATCCGCAGCCAGGAGCTA 1098
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   116 ACCGGGGAGCGGAGCCGGCTGCTCACCTACGTGCAGGACTACCTTGAGTGCGTGGAG 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   918
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    355
                                                                                                                                                                                                                                                                                                                                                                              the p53 pathway occurs in a much larger proportion of the p53 gene ramains unknown but p53 has been found to act in cooperation with many cases the mechanism of functional inactivation of the p53 gene remains unknown but p53 has been found to act in cooperation with 1001 in cooperation between ING1 and p53 suggested that ING1. Functional cooperation between ING1 and p53 suggested that ING1 mechanism of the ing1 in head and neck cancers and chromosomal location of the ING1 placed it within a region that is frequently rearranged in head and neck cancers and chromosomal location of the ING1 in head and neck cancers and chromosomal location of the ING1 in head and neck cancers and chromosomal location of the ING1 in head and neck cancers and suggesting that ing1 revealed mutations in ING1 nor significant variations in its cancer elology. However, alternative initiation exons of the ing1 cancer elology. However, alternative initiation exons of the ing1 gene, each having that rown promoter have been discovered.

Expression of one promoter (la) produces a protein having on identical C-terminal fragment to ING1 but an additional 104 of ing1 mindentical C-terminal fragment to ING1 but an additional 104 of ing1 mindentical condentinal fragment to ING1 but an additional 104 of ing1 mose expressing wild type p53 p37NG1 is able to cause proliferation of an oncogene. When overexpressed in cells (even tharacteristics of an oncogene. When overexpressed in cells condenting expressing the concept of ing1 by hybridisation with an outles and encoding exon 10 of ing1 by hybridisation with an outles of encoding exon 10 of ing1 by hybridisation with an outles and encoding exon 10 of ing1 by hybridisation with an original peptide of p37ING1 can also be used to raise antibodies that can also be used in detection methods for the p37ING1 variant. The polypeptides may be useful in gene therapy for treatment of cell erigin expressing and encoding expressing the detection methods for the p37ING1 expressing and expressing expressing expressi
                                                                                                                                                                                            Detecting nucleic acid encoding exon 1b of ing1, useful for diagnosing and treating cancer, comprises contacting sample with isolated nucleic acid comprising sequence of exon 1b and detecting hybridized products
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               176 TCGCTGCCCCACGACATGCAGGAACGTGTCTGTGCTGCGAGAGGTGGACAAATAT
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                                                                                                                                                                                                                                                                                                                                        Mutations in or loss of the p53 gene occur in more than 50% of human tumours and tumour cell lines, but functional inactivation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23.5%; Score 253.6; DB 21; Length 2817;
1larity 60.3%; Pred. No. 5.7e-48;
Conservative 0; Mismatches 289; Indels 33;
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nes 289;
                                                                         Grigorian IA;
                                                                       Gurova KV,
                                                                                                                                                                                                                                                                                             Disclosure; Fig 11; 134pp; English.
                      UNII ) UNIV ILLINOIS FOUND.
                                                                       Zeremski M,
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                                                                                                                                                              805
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                                                219 GGCAGCGGCAAGGCGGGCCAGGACAAGTCGAAGAGTGAGGCCATCACACGCAGATAAG
                CAGGTGGACAGTGAGGTCTTTCGAAGCACACCAGGACATCAGTGACGCCACTGGT
                                    -----GTGAACGAGCCTCAGATAAAGCAAAGATGGATTCCAGCCAACCAGAAAGATCT
                                                                          GACCCCCCCAGCAGCGACCAGTGAAAGCCGTGATTTATGTCACATG
                                                                                                              GCAAATGGGATTGAAGACTGTGATGATCAGCCACCTAAAGAAAAGAAATCCAAGTCAGCA
                                                                                                                                 AATCACGACCATGATGACATCACCTCAGGAACGCCCAAGGAGAAGAAAGCAAAAACCTCA
                                                                                                                                                    AAGAAAAAGAAACGCTCCAAGGCCAAGCAGAAAGGGAAGCTTCACCTGTTGAGTTTGCA
                                                                                                                                                                                          ATAGATCCTAATGAACCTACATACTGCTTATGCAACCAAGTGTCTTATGGGGAGATGATA
                                                                                                                                                                                                                              GGATGTGACAATGGACAGTGTCCAATTGAATGGTTTCACTTTTCATGTGTTTCACTTACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                    p53; tumour; cancer; detection; antibody; hybridisation; exon 1b; ING1; ing1; p33ING1; p37ING1; oncogene; gene therapy; diagnosis; proliferation disorder; transformation; transformed cell; human;
CAAATGGAGTTACACTCACAGTGTTTCCAAGATCCTGCTGAAA
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                                                                                                                                                                                                                                                                                                         GACAAAAGTACTGAAAAGACAAAAAAGGATAG
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145 205 265 476 445 264 324 384 325 444 385 534 594 565 654 human tumours and tumour cell lines, but functional inactivation of the p53 pathway occurs in a much larger proportion of the p53 gene remains unknown but p53 has been found to act in cooperation with INGI. Functional cooperation between INGI and p53 suggested that INGI encoded a tumour suppressor protein that functional within the p53 pathway. This data suggested a possible role for INGI head within the p53 pathway. This data suggested a possible role for INGI head within the p53 pathway. This data suggested a possible role for INGI head and neck cancers and chromosomal location of the INGI placed it within a region that is frequently rearranged in head and neck cancers. Large scale analysis of tumours involving INGI has not revealed mutations in INGI nor significant variations in its expression suggesting that INGI was not a useful gene to study in cancer etiology. However, alternative initiation exons of the ingicane, each having their own promoter have been discovered. Expression of a second promoter (1b) produces a protein has been identical c-terminal fragment to INGI but an additional 104 N-terminal anino acids. The newly discovered protein has been characteristics of an oncogene When overexpressed in cells (even those expressing wild type; p33INGI). p37INGI has the characteristics of an oncogene. When overexpressed in cells cancer choiceration or transformation of those cells. Thus detecting a proleic acid encoding exon 1b of ingl by hybridisation with an isolated nucleic acid having the sequence of exon 1b of ingl the GCGCCAGCAGCAGCTGGGCGACAGGTGGGCAACAGCGGCAAGGTTGGCGCGGACAGGCC 266 GCAGCGCGCGCTGATCCGCAGCAGCAGCAGGAGAAGATCCAGATCGTGAGCCA ------CTGCTGAAAGTGAACGAGCCTCAGATA 86 CTATGTGGAGGACTACCTGGACTCCATCGAGTCCCTGCCTTTCGACTTGCAGAAATGT GTCTGTGCTGCGAGAGCTGGACAACAAATATCAAGAAACGTTAAAGGAAATTGATGTT 385 AATGCTCGAATTGGTGGAAAATCGGGCAAGACAAATGGAGTTACACTCACAGTGTTTCCA AAGCAAAGATGGATTCCAGCCAACCAGAAAGATCTTCAAGAAGACCCCGCAG--GCAGCG 446 CAATGGCGATGCGGTAGCGCAGTCTGACAAGCCCAACAGCGAAGCGCTCACGGCGGCGCAGCG GACCAGTGAAAGCCGTGATTTATGTCACATGGCAAATGGGATTGAAGACTGTGATGATCA CAACAACGAGAACCGTGAGAACGCGTCCAGCAACCACGACCACGACGACGCCCTCGGG GCCACCTAAAGAAAAGCCAAGTCCAAGTCAGCAAAGAAAAGGAAACGCTCCAAGGCCAAGCA CTACGAAAAATATAAGAAAGAAGATGATTTAAAACCAGAAGAAAGGTCTACAGCAGCTTCT 206 CTACGAGCGCTTCAGTCGCGAGACAGACGGGGCGCGGAAGCGGCGGATGCTGCACTGTGT CTACGTGCAGGACTACCTTGAGTGCGTGGAGTCGCTGCCCCACGACGTGCAGAGGAACGT Gaps or its antisense sequence can identify individuals expressing the oncogenic form of ingl. Novel peptide sequences taken from the 104 Noterminal peptide of p37ING1 can also be used to raise antibodies that can also be used in detection methods for the p37ING1 variant The polypeptides may be useful in gene therapy for treatment of cel. 30; Length Indels Sequence 911 BP; 228 A; 255 C; 305 G; 123 T; 0 other; The polypeptides may be useful in gene therapy for t proliferation disorders, especially cancers and for DB 21; Score 237.4; DB 21, Pred. No. 1.9e-44; ; 0 22.0%; Conservative 445 AGATC-----Similarity cancers.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cancer associated antigen; ING1; tumour suppressor; cancer; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cancer associated nucleic acid molecule identified by SEREX ical identification of antigens by recombinant expression technique, useful in nucleic acid based therapies to treat
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cancer associated antigen"
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(SLOK ) SLOAN KETTERING INST CANCER RES.
(CORR ) CORNELL RES FOUND INC.
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The present sequence encodes a human cancer associated antigen. The sequence is a variant of the ING1 gene, which is a tumour suppressor gene candidate. The cancer associated antigen polynucleotides and polypeptides are useful for screening for the possible presence of a pathological condition in a subject such as cancer. The cancer associated antigen polypeptides are useful for producing vaccines.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    145 CTACGTGCAGGACTACCTTGAGTGCGTGGAGTCGCTGCCCCACGACATATGCAGAGGAACGT
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                                                                                                                                                                                                                                                                                                                                                          CTATGTGGAGGACTACCTGGACTCCATCGAGTCCCTGCCTTTCGACTTGCAGAAATGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTACGAAAAATATAAGAAAGAAGATGATTTAAAACCAGAAGAAACGTCTACAGCAGCTTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TATGCAACCAAGTGTCTTATGGGGAGATGATAGGATGTGACAATGAACAGTGTCCAATTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AATGGTTTCACTTTTCATGTGTTTCACTTACCTATAAACCAAAGGGGAAATGGTATTGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CAAAGTGCAGGGGAGATAATGAGAAAACAATGGACAAAAGTACTGAAAAGGACAAAAAGG
                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                               32;
                                                                                                                                                                                                              Length 1533;
                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                    Sequence 1533 BP; 336 A; 431 C; 521 G; 244 T; 1 other;
                                                                                                                                                                                                                                                               0; Mismatches 290;
                                                                                                                                                                                                                 Score 236; DB 22;
Pred. No. 4.7e-44;
                                                                                                                                                                                                                 21.9%;
58.9%;
                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                            Similarity
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1633 CCAAGTGCCGGGGGGAGAAGAGAGAGAGAGAAAGCCCTGGAGAAATCCAAAAAG 1692
                                                                                                1573 AGTGGTTCCACTTCTCGTGGGGCTCAATCATAAACCCAAGGGCAAGTGGTACTGTC 1632
                                                                                                                                                                                                                                                                                            .094 GCAGCGCGCGCTGATCCGCAGCCAGGAGCTGGGCGAGGAAGATGTCGATCGTGAGCCA 1153
                                                                                                                                                                                                                                                                                                                                                                                                      1154 GATGGTGGAGCTGGTGGAGAACCGCACGCGCAGGTGGACAGCCACGTGGAGCTGTTCGA 1213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1214 GGCGCAGCAGCAGCTGGGCGACACAGCGGCAACAGCGGCAAGGCTGGCGGGACAGGCC 1273
  1393 GCACACCCAAGGAGAAGAAGGCCAAGAAGAAGAAGAAGCGCTCCAAGAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     654 AGGAAAGGGAAGCTTCACCTGTTGAGTTTGCAATAGATCCTAATGAACCTACATACTGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GTCTGTGCTGCGAGAGCTGGACAACAAATATCAAGAAACGTTAAAAGGAAATTGATGATGT
                                                                                                                                                                   265 CTACGAAAAATATAAGAAAGAAGATGATTTAAACCAGAAGAAACGTCTACAGCAGCTTCT
                                                                                                                                                                                                                  1034 CTACGAGCGCTTCAGTCGCGAGACAGACGGGGCGCAGAAGCGGCGGGTGCTGCACTGTGT
                                                                                                                                                                                                                                                                                                                                                            385 AATGCTCGAATTGGTGGAAAATCGGGCAAGACAAATGGAGTTACACTCACAGTGTTTCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                       445 AGATC-----CTGCTGAAAGTGAACGAGCCTCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            534 GGACCAGTGAAAGCCGTGATTTATGTCACATGGCAAATGGGATTGAAGACTGTGATGATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1333 GCAACAACGAGAACCGTGAGAACGCGTCCAGCAACCACGACGACGACGGCGCCCTCGG
                                                                                                                                                                                                                                                                 714 TATGCAACCAAGTGTCTTATGGGGAGATGATAGGATGTGACAATGAACAGTGTCCAATTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AATGGTTTCACTTTTCATGTGTTTCACTTACCTATAAACCAAAGGGGAAATGGTATTGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CAAAGTGCAGGGGAGATAATGAGAAAACAATGGACAAAAGTACTGAAAAAGACAAAAAAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                p53; tumour; cancer; detection; antibody; hybridisation; exon 1b; ING1; ing1; p331NG1; p371NG1; oncogene; gene therapy; diagnosis; proliferation disorder; transformation; transformed cell; mouse; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Murine ingl common exon sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CDNA; 1835
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAA53789 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention discloses monoclonal antibodies which can be used, in combination, to specifically recognise epitopes of ING1 (inhibitor of growth 1) protein isoforms. ING1 is a tumour suppressor gene and its expression is regulated through the cell cycle, peaking in the S phase. Expression of ING1 is down regulated in breast tumours and lymphoid malignancies. Overexpression of a construct containing the ING1 pene is able to inhibit cell growth by reducing the fraction of cells which enter into the S phase. The monoclonal antibodies are useful for detecting an ING1 protein in a cell, which involves selecting a cells that ectopically or endogenously expresses ING1 protein. The anti-ING1 monoclonal antibody combination consists of two or more antibodies of CAD1-CAD10 (not defined), preferably a mixture of CAD1-CAD4, which can detect at least two different isoforms of ING1. The antibodies are also useful for diagnosing a disease e.g. tumour or medical condition in an animal preferably, human) associated with aberrant levels of an ING1 protein. The sequence presented is the human inhibitor of growth I (ING1) isoform, protein used to raise antibodies.
                                                                                                                                                                                                                    malignancy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel monoclonal antibody which specifically recognizes epitope of ING1, inhibitor of growth 1 protein, and designated CAb1-10, useful for detecting two different isoforms of ING1 and diagnosing a medical condition
                                                                                                                                                                     Human, gene; ss; monoclonal antibody; epitope; inhibitor of growth 1;
ING1; tumour suppressor; cell cycle; breast tumour; lymphoid malignan
cell growth; anti-ING1; CAb; isoform; diagnosis; tumour; antigen;
p331NG1b.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21.9%; Score 236; DB 24; Length 2897; 58.9%; Pred. No. 6e-44; iive 0; Mismatches 290; Indels 32
                                                                                                                                       Human inhibitor of growth 1 (ING1) isoform, p33ING1b, cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2897 BP; 733 A; 710 C; 819 G; 635 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 10-12; 15pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                               /product- "p33ING1b
                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
873..1712
ABK86977 standard; cDNA; 2897
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9605-0751230.
9505-0569721.
200005-0532868.
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                                                                                           (first entry)
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Matches 462; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Riabowol KT, Boland D;
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BOLAND D.
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                                                                                                                                                                                                                                                                                                           Homo sapiens.
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                                                                                           24-SEP-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            36-FEB-1999;
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(BOLA/) 1
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WO200046370-A1

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P-PSDB; AAB84697
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nutations in or loss of the p53 gene occur in more than 50% of human tumours and tumour cell lines, but functional inactivation of human tumours and tumour cell lines, but functional inactivation of the p53 pathway occurs in a much larger proportion of the p53 gene remains unknown but p53 has been found to act in cooperation with remains unknown but p53 has been found to act in cooperation with the remains unknown but p53 has been found to act in cooperation with right endicated cooperation by the remains unknown but p53 has been found to act in cooperation with right endicated a tumour suppressor protein that functioned within the p53 pathway. This data suggested a possible role for ING1 in head and neck cancers and chromosomal location of the ING1 placed it within a region that is frequently rearranged in head and neck cancers. Large scale analysis of tumours involving ING1 has not within a region that is frequently rearranged in head and neck cancer etiology. However, alternative initiation exons of the ing1 expression suggesting that ING1 mas not a useful gene to study in cancer etiology. However, alternative initiation exons of the ing1 ene, each having their own promoter have been discovered. Expression of one promoter (1a) produces a protein land of the ing1.

Expression of one promoter (1a) produces a protein having an identical C-terminal fragment to ING1 but an additional 104 networe expression of a second promoter (1b) p37ING1 has the characteristics of an oncogene. When overexpressed in cells (even those expressing wild type p33 p7ING1; ability the cancer of exon 1b of ing1 by hybridisation with an isolated nucleic acid encoding exon 1b of ing1 by hybridisation with an isolated nucleic acid encoding exon 1b of ing1 by hybridisation with an isolated nucleic acid maving the sequence of exon 1b of ing1 or its antisense sequence can identify individuals expressing the cancer in identify individuals expressing the polypeptides may be useful in gene therapy for treatment of cell studies and be used in det
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7 TGAAGGAGCTGGACGACTACTATGAGAAGTTCAAACGGGAACAGACGGCACCCAGAAAGC 66
                                                                                                                                                                                                         Detecting nucleic acid encoding exon 1b of ingl, useful for diagnosing and treating cancer, comprises contacting sample with isolated nucleic acid comprising sequence of exon 1b and detecting hybridized products
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       306 AACGTCTACAGCAGCTTCTCCAGAGAGCACTAATTAATAGTCAAGAATTGGGAGATGAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAATACAGATTGTTACACAAATGCTCGAATTGGTGGAAAATCGGGCAAGACAAATGGAGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
18.3%; Score 197.2; DB 21; Length 1835;
Best Local Similarity 58.5%; Pred. No. 3.5e-35;
Matches 399; Conservative 0; Mismatches 253; Indels 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1835 BP; 541 A; 387 C; 468 G; 439 T; 0 other;
                                                                                                                                              Grigorian IA;
                                                                                                                                                Gurova KV,
                                                                                                                                                                                                                                                                            Claim 17; Fig 6; 134pp; English.
                                                                              99US-0118941.
                                              04-FEB-2000; 2000WO-US02959
                                                                                                              (UNII ) UNIV ILLINOIS FOUND
                                                                                                                                                Zeremski M,
                                                                                                                                                                            WPI; 2000-491278/43.
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                                                                              04-FEB-1999;
                10-AUG-2000
                                                                                                                                            Gudkov A,
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521
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cancer associated antigen; ING1; tumour suppressor; cancer; vaccine; ss.
                                                                                                         247 AGGCGGCCCAGGACAAGTCGAAGAGTGAGGCCATCACACAGGCAGATAAGACCGAATAACA
                                                                                                                                                            576 TTGAAGACTGTGATGATCAGCCACCTAAAGAAAAGAAATCCAAGTCAGCAAAGAAAAGA
                                                                                                                                                                                                                                                                                                                                                                   487 ACGAGCCCACGTACTGTCTGTGCAACCAGGTCTCCTACGGGGAGATGATCGGCTGTGACA
                                                                                                                                                                                                                                                                                                                                                                                                           ATGAACAGTGTCCAATTGAATGGTTTCACTTTCATGTGTTTTCACTTACCTATAAACCAA
                                                                                -----CCCGCAGGCAGCGGACCAGTGAAAGCCGTGATTTATGTCACATGGCAAATGGGA
                                                                                                                                                                                                                                               AACGCTCCAAGGCAAGCAGGAAAGGCAAGCTTCACCTGTTGAGTTTGCAATAGATCCTA
                                                                                                                                                                                                                                                                                                                             463 ACGAGCCTCAGATAAAGCAAAGATGGATTCCAGCCAACCAGAAAGATCTTCAAGAAGAC-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleotide sequence of a human cancer associated antigen.
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/transl_except= "(pos: 25..30, aa: Cys)"
/transl_except= "(pos: 124..126, aa: Pro./poroduct= "cancer assocciated antigen"
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(SLOK ) SLOAN KETTERING INST CANCER
(CORR ) CORNELL RES FOUND INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          876 CTGAAAAGACAAAAAAGGATAG 897
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24-OCT-2000; 2000US-0602362.
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ING1; p33ING1; breast cancer; brain cancer;

Location/Qualifiers 109..741 /*tag= a

INC

96WO-CA00819 96US-0751230 95US-0569721

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Tumour suppressor gene ING1 partial cDNA
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                                                              Tumour suppressor gene; ING; diagnosis; gene therapy; ss.
                      (first entry)
                                                                                             sapiens
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08-DEC-1995;
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  AAT69651;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GATGTGACAATGAACAGTGTCCAATTGAATGGTTTCACTTTTCATGTGTTTCACCTTAACCT 806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               853
                                                                               The sequence is the wildtype of the ING1 gene, which is a tumour suppressor gene candidate. The cancer associated antigen polynucleotides and polypeptides are useful for screening for the possible presence of a pathological condition in a subject such as cancer. The cancer associated antigen polypeptides are useful for producing vaccines.
                                                                                                                                                                                                                                                                                                                                                                                                                            CCAACAGCAAGCGCTCACGGCGGCAGCGCAACCAACAACGCTGAGCAACGCTCCAGCA
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                                                                                                                                                                                                                                                                                                                                                                          -CTGCTGAAAGTGAACGAGCCTCAGATAAAGCAAAGATGGATTCCAGCCAACCAGAAAGA
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                                                                                                                                                                                                                                                                                                                                                                                                                TCTTCAAGAA - - GACCCCGCAGGCAGCGACCAGTGAAAGCCGTGATTTATGTCACATGG
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cer associated nucleic acid molecule identified by SEREY identification of antigens by recombinant expression bnique, useful in nucleic acid based therapies to treat
                                                                                                                                                                DB 22; Length 1143;
                                                                                                                                                                                     30;
                                                                      sequence encodes a human cancer associated antigen
                                                                                                                                                              tch
al Similarity 57.0%; Score 183.8; DB 22; Length
al Similarity 57.0%; Pred. No. 3.4e-32;
394; Conservative 0; Mismatches 267; Indels
                                                                                                                                            Sequence 1143 BP; 289 A; 291 C; 366 G; 197 T; 0 other;
                                                                                                                                                                                                                                                                                                                                AAATGGAGTTACACTCACAGTGTTTCCAAGATC-----
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                                                  62pp; English,
                                                  Example 4; Page 44;
                    technique,
                                                                                                                                                                         Local Similarity
  cancer
          (serological cloning) tech
                                                                     The present
The sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                          hybridisation between normal mammary and transformed epithelial CDNAs, isolation of an antisense ING1 CDNA insert that caused increased cell proliferation, and use of the insert to screen normal human fibroblast and HeLa CDNA libraries. A complete ING1 sequence (AAT69652) was obtd. by 5'RACE. ING1 is localised to the 13433-34 chromosome region, to which a number of human cancers have been mapped. ING1 nucleic acids can be used in the diagnosis of breast cancer; a decreased level of ING1 mRNA indicates cancerous cells. They can also be used in gene therapy methods to block the
                                                                                                                                                                                                                                                                                                                               novel
                                                                                                                                           Isolated tumour suppressor gene, ING1 - useful to develop products for inhibiting or increasing cell proliferation, in particular for treatment or diagnosis of cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 18; Length 1902;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30;
                                                                                                                                                                                                                                                                                                                      A partial cDNA clone (AAT69651), designated ING1, codes for a tumour suppressor protein p331NG1 (AAW19118) that is a potent inhibitor of cell growth. It was isolated by subtractive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 183.8; DB 18; Length
Pred. No. 4.1e-32;
0; Mismatches 267; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1902 BP; 574 A; 391 C; 461 G; 476 T; 0 other;
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                                                                                                                                                                                                                                                                    Claim 1; Fig 2; 63pp; English
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Local Similarity 57.0%;
hes 394; Conservative
Garkavstev I, Riabowol
                                                    WPI; 1997-332781/30.
                                                                                   P-PSDB; AAW19118
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                       ACAGCGGCAAGGTTGGCGCGGACAGGCCCAATGGCGATGCGGTAGCGCAGTCTGACAAGC 334
                                                                                                          AGAAGAAGAAGCGCTCCAAGGCCAAGGGGGGAGGAAGAAGAAGACGCCCTGCCGCACCTCCCCA
                                                                                                                                                                                                                                                 -CTGCTGAAAGTGAACGAGCCTCAGATAAAGCAAAGATGGATTCCAGCCAACCAGAAAGA
                                                                                            CAAATGGGATTGAAGACTGTGATGATCAGCCACCTAAAGAAAAGAAATCCAAGTCAGCAA
                                                                                                                                           AGAAAAAGAAACGCTCCAAGGCCAAGCAGGAAAGGGAAGCTTCACCTGTTGAGTTTGCAA
                                                                                                                                                                                                                                    GATGTGACAATGAACAGTGTCCAATTGAATGGTTTCACTTTTCATGTGTTTCACTTACCT
                                               TCTTCAAGAA - - GACCCCGCAGCGGACCAGTGAAAGCCGTGATTTATGTCACATGG
                                                                                                                                                                                                                                                                                  ATAAACCAAAGGGGAAATGGTATTGCCCAAAGTGCAGGGGAGATAATGAGAAAACAATGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Modulating eukaryotic apoptosis by increasing p33ING1 activity -using p33ING1 derivatives, to induce apoptosis in cancer cells, and in the investigation of apoptotic pathways
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          human; apoptosis; cell death; breast cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Johnston RN, Riabowol K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    orain tumour; gene therapy; tumour suppressor; ss.
                                                                                                                                                                                                                                                                                                                                            ACAAAAGTACTGAAAAGACAAAAAAGGATAG 897
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109..741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Partial ING1 partial cDNA sequence.
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P-PSDB; AAW79674.
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CGCAGAAGCGGCGGATGCTGCTGTGTGCAGCGCGCGCTGATCCGCAGGAGCTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    eukaryotic cell, an assay for determining the level of p33ING1 activity in a eukaryotic cell, and an isolated eukaryotic cell substantially free of p33ING1 biological activity. The invention discloses ING1 derivatives or variants that may be used to induce
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GATGTGACAATGAACAGTGTCCAATTGAATGGTTTCACTTTTCATGTGTTTCACTTACCT 806

747

TAGATCCTAATGAACCTACATACTGCTTATGCAACCAAGTGTCTTATGGGGAGATGATAG INGI nucleic acids can a decreased level of can also be used in gene of cancer cells.

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Sequence 2061 BP; 602.A; 439 C; 515 G; 505 T; 0 other;
                       be used in the diagnosis of breast cancer;
ING1 mRNA indicates cancerous cells. They
therapy methods to block the proliferation
      number of human cancers have been mapped.
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                                         novel 33 NDa tumour suppressor protein p33ING1 (AAW1919), formerly p33IG1, that is a potent inhibitor of cell growth. A partial clone (AAT69651) was isolated by subtractive hybridisation between normal mammary and transformed epithelial cDNAs, isolation of an antisense ING1 cDNA insert that caused increased cell proliferation, and use of the insert to screen normal human fibroblast and HeLa CDNA ilbraries. The complete ING1 sequence was then obtd. by 5'RACE. ING1 is localised to the 13q33-34 chromosome region, to which a
                                                                                                                                                                                                                                                                                                                                                                                                                                           gene; ING1; p33ING1; breast cancer; brain cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Isolated tumour suppressor gene, INC1 - useful to develop products for inhibiting or increasing cell proliferation, in particular for treatment or diagnosis of cancer
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17.0%; Score 183.8; DB 18; Length 2061; 57.0%; Pred. No. 4.2e-32;
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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nu	nucleic search, using sw model
Run on:	June 20, 2003, 01:19:25 ; Search time 2824 Seconds (without alignments) 11129.968 Million cell updates/sec
Title: Perfect score: Sequence:	US-09-513-365A-2 1080 1 gcggccgcggtgcatgaaaaaaaaaaaaaaaaa 1080
Scoring table:	IDENTITY_NUC Gapop 10:0 , Gapext 1.0
Searched:	2054640 segs, 14551402878 residues
Total number of	hits satisfying chosen parameters: 4109280
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                                                                              Mismatches
               1. .1080
/organism="Homo sapiens"
/db_xref="taxon:9606"
/note="p331NG2"
a 196 c 271 g 238
SECRETARY OF THE DEPARTMENT OF
                                           238
       Location/Qualifiers
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Best Local Similarity
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/translation="MLGQQQQLYSSAALLTGERSRLLTCYVQDYLECVESLPHDMQRNVSVLRELDNKYQETLKEIDDVYEKYKKEDDLAGKRLQQLLQRALINSQELGDEKIQ IVTQMLELVENTRRQWELHSQCFQDPAESERASDKKMLQQLQRALINSQELGDEKIQ IVTQMLELVENTRRQWELSCSQPERSSRPRQRTSES FDLCHMANGIEDCDDQPPKEKKSKGARKKKRSKAKQBREASPVERIDPNEPTYCLCN QVSYGEMIGCDNEQCPIEWFHFSCVSLTYKPKGKWYCPKCRGDNEKTMDKSTEKTKKD RRSR"
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                ATCGAGGTAGTAAAGGCCATCCACATTTTAAAGGGTTATTGTCTTTTATATAATTCGTT
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Nagashima, M., Shiseki, M., Miura, K., Hagiwara, K., Linke, S.P., Pedeux, R., Wang, X. W., Yokota, J., Riabowol, K. and Harris, C.C. DNA damage-inducible gene p331NG2 negatively regulates cell proliferation through acetylation of p53
Proc. Natl. Acad. Sci. U.S.A. 98 (17), 9671-9676 (2001)
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Nagashima, M., Hadiwara,K., Minter,A.R. and IDirect Submission
Submitted (12-MAR-1998) Laboratory of Human
National Cancer Institute, 37 Convent Drive
Bethesda, MD 20892, USA
Location/Quallifiers
                                                                                                                                                                                                                                          AF053537 1080 bp mRNA
Homo sapiens p33 (ING2) mRNA, complete cds.
AF053537
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.larity 100.0%; Pred. No. 3.1e-222;
Conservative 0; Mismatches 0;
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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/note="polymorphism"
/replace="c"
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CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing Dy: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: http://www.nisc.nih.gov/
Contact: nisc_mgc@nhgri.nih.gov/
Rkhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C.,
Blakesley,R.W., Ganite,S., Guan,X., Gupta,J., Haghighi,P.,
Hansen,N., Ho,S.-L., Karling,E., Laric,P., Legaspi,R., Maduro,Q.L.,
Masiello,C., Maskeri,B., Mastrian,S.D.,McCloskey,J.C., McDowell,J.,
Pearson,R., Stantripops,S., Thomas,P.J., Touchman,J.W., Tsurgeon,C.,
Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L., Young,A.,
Zhang,L.-H. and Green,E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /translation="MGGQQQQLYSSAALLTGERSRLLTCYQDYLECVESLPHDMQR
NVSYLRELDNKYOETLKEIDDYYEKYKREDDLNQKRRLQQLLQRALINSQELGDEKIQ
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RDLCHMANGIEDCDOPPREKSKGAKKKRSRAKQEREASFYEFAIDPNEFYCLCN
OVSYGEMIGCDNEQCPIEWFHFSCVSLTYKPKGKWYCPKCRGDNEKTMDKSTEKTKKD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Clone distribution: MGC clone distribution information can be four through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAL Plate: 15 Row: m Column: 11
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA g1: 4504694.
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                                                                                                       Euteleostomi;
                                                                                                                                                                       Direct Submission
Submitted (07-MAY-2002) National Institutes of Health, Mammalian
                                                                                                                                                                                                        Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 GCGCCGCGCCGCTGCATGTGCGGCTGCTGGATGCGGAGGCGGCGCGGCGCGCGGAT
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Primates; Catarrhini; Hominidae;
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/clone_lib="NIH_MGC_7"
/lab_host="DH10B-R"
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     cds
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/db_xref="LocusID:3622"
/db_xref="LocusID:3627"
/db_xref="MGC:10524 IWAGE:3941655"
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Mismatches 0
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     mRNA,
                                                                                                                                                                                                                                                                                          Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
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MGC:10524 IMAGE:3941655,
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                                   GI:20987212
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Mammalia; Eutheria;
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                                                                                     TAAAGAAAAGAAATCCAAGTCAGCAAAGAAAAGAAAGCGCTCCAAGGCCAAGGAAAG
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CGGCAGGATGTTAGGGCAGCAGCAGCAACTGTACTCGTCGGCTGCGCTCCTGACCGG
                                                                   GGAGCGGAGCCGGCTGCTCACCTGCTACGTGCAGGACTACCTTGAGTGCGTGGAGTCGCT
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Homo sapiens, inhibitor of growth family, member 1-like, clone
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QVSYGEMIGCDNEQOPIEWFHFSCVSLLYKPKGKWYCPKCRGDNEXTMDKSTERTKKD
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                                                                          Craniata; Vertebrata; Euteleostomi;
Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                          Shimaday.r., Saito, A. and Horie, M. C. Direct Submission
Submitted (07-APR-19989-Yoshikazu Shimada, Otsuka Pharmaceutical
Co. Led., Otsuka GEN Research Institute; Kagasuno, Kawauchi-cho,
Tokushima, Tokushima 771-0192, Japan
(E-mail:shim@otsuka.genome.ad.jp, Tel:81-886-65-2888(ex.2476),
                                                                                                                                Horie,M.
L, a candidate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGAGCGGAGCCGGCTCACCTGCTACGTGCAGGACTACCTTGAGTGCGTGGAGTCGCT
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                                         to mRNA
                                                                                                                            Shimada,Y., Saito,A., Suzuki,M., Takahashi,E. and Hori
Cloning of a novel gene (INGIL) homologous to ING1, a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 1078;
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                                     Homo sapiens fetal tissue_lib:fetal-brain cDNA
Homo sapiens
                                                                                                                                                                                   Cytogenet. Cell Genet. 83 (3-4), 232-235 (1998) 99172097
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99.5%; Pred. No. 6.5e-215;
ive 0; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                      Sequence updated (17-Apr-1998).
Location/Qualifiers
1. 1078
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1. 1078
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                                                                       Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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GI:4115554
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Best Local Similarity
Matches 1049; Conserv
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PRI 18-MAR-1999

1078 bp mRNA linear

AB012853 Homo sapiens ING1L AB012853

LOCUS DEFINITION ACCESSION RESULT 4 AB012853

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QVSYGEMIGGDNEQCPIEMFFRSCVSLTYKEKGKWYCPKCRGDNEKTMDKSTEKTKKD
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Pred. No. 1.6e-170;
); Mismatches 2;
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99.8%;
                                        /gene="ing2"
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                     CCAAGTGTCTTATGGGGAGATGATAGGATGTGACAATGAACAGTGTCCAATTGAATGGTT
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          TGAAAAAATACAGATTGTTACACAAATGCTCGAATTGGTGGAAAATCGGGCAAGACAAAT
                                                  GGAGTTACACTCACAGTGTTTCCAAGATCCTGCTGAAAGTGAACGAGCCTCAGATAAAGC
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Submitted (08-JUN-1998) Lopez-Otin C., Bioquimica y Biologia
Molecular, Universidad de Oviedo. Facultad de Medicina., C/ J
Claveria s/n, 33006, SPAIN
1. e43
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Cal,S., Freije,J.M. and Lopez-Otin,C.
ING2,a new possible gene supressor tumor
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AJ006851
AJ006851.1 GI:12053587
ing2 gene; p32 protein.
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AC107214 10-APR-2002 Homo sapiens chromosome 4 clone RP11-367N14, WORKING DRAFT SEQUENCE, 8 unordered pieces.
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Waterston R.H.
Direct Submitssion
Submitted (16-JAN-2002) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
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Catarrhini; Hominidae; Homo.
 237 TTGGGAGATGAAAAATACAGATTGTTACACAAATGCTCGAATTGGTGGAAAATCGGGCA
                                                                                                                                                 AATTCGTTTGCTTTCAGAAATGTTTTAGGGTAAATGCATAAGACTATGCAATAATTTTT
                                                                                                                               AGACAAATGGAGTTACACTCACAGTGTTTCCAAGATCCTGCTGAAAGTGAACGAGCCTCA
                                                                                                                                                                                                      533 CGGACCAGTGAAAGCCGTGATTTATGTCACATGGCAAATGGGATTGAAGACTGTGAFGAT
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HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
Homo sapiens.
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Mammalia; Eutheria; Primates;
1 (bases 1 to 189972)
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/db_xref="G1:9992842"
/db_xref="G1:999284"
/db_xref="G1:99
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Catarrhini; Hominidae; Homo.
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Location/Qualifiers
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; H
1 (bases 1 to 974)
Nagashima, M., Hagiwara,K., Minter,A.R. and Harris,C.C.
Direct Submission
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/pin AF062147.1:68. .239,124. .794)
/gene="ING2"
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/db_xref="taxon:9606"
order(AF062747.1:1. 423,1. .938)
/gene="iNG2"
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/gene="ING2"
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/gene="ING2"
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11 Similarity 99.6%;
819; Conservative
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/note="assembly_name:Contig66
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/note="assembly_name:Contig67
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                                                                                                                            Louis,
Mo 63108, USA
3 (bases 1 to 189972)
Waterston, R.H.
Direct Submission
Submitted (10-APR-2002) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St.
Mo 63108, USA
On Apr 10, 2002 this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          * NOTE: This is a 'working draft' sequence. It currently consists of 8 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                             Sequencing vector: plasmid; 100%
Sequencing vector: plasmid; 100%
Chemistry: Dye-primer ET; 0% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 189641 bases at least Q40
Consensus quality: 199699 bases at least Q20
Consensus quality: 199699 bases at least Q20
Insert size: 1204000; agarose-fp
Insert size: 120574; sum-of-contiss
Quality coverage: 11.39 in Q20 bases; sum-of-contiss
Quality coverage: 10.96 in Q20 bases; sum-of-contiss
                                                                                                                                                                                                             Center: Washington University Genome Sequencing Center
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contig of 1847 bp in length
app of unknown length
contig of 1121 bp in length
gap of unknown length
contig of 1138 bp in length
gap of unknown length
contig of 1108 bp in length
contig of 1108 bp in length
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37117: contig of 30151 bp in length
37217: gap of unknown length
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known length
88470 bp in length
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Anote-"assembly_name:Contig44"
4521. .5658
/note-"assembly_name:Contig56"
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1353. :3199
/note="assembly_name:Contig29"
3300. :4420
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/note="assembly_name:Contig58"
6967. .37117
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/note="assembly_name:Contig65"
37218. .101402
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    Summary Statistics

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/db_xref="taxon:9606"
/chromosome="4"
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147065 CAGCCACCTAAAGAAAAGAAATCCAAGTCAGCAAAGAAAAAAGAAAAGGCTCCAAGGCCAAG 147124
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                                                                                                                                    233 TATCAAGAAACGTTAAAGGAAATTGATGATGTCTACGAAAAATATAAGAAGAAGATGAT
                                                                                                                                                                                                                  413 AGACAAATGGAGTTACACTCACAGTGTTTCCAAGATCCTGCTGAAAGTGAACGAGCCTCA
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                                                                                                                                                                                                                                                                                              353 TTGGGAGATGAAAAATACAGATTGTTACACAAATGCTCGAATTGGTGGAAAATCGGGCA
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                                                     Score 817.2; DB.2;
Pred. No. 3.8e-165;
0; Mismatches 3;
54950 t
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099 777 720 837 780

540 657 900

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658 AAGGGAAGCTTCACCTGTTGAGTTTGCAATAGATCCTAATGAACCTACATACTGCTTATG
                                                                                                               601 GAGGGAGGCATCCTGTGGAGTTTGCCATCGATCCCAATGAGCCCCACCTACTGCTTGTG
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/db_xref="G1:10039543"
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SRDLCHWTNGIDDCDDQPPKEKRSKSAKKKRSKAKQEREASSVERIDPNEPYYCLC
NQVSYGEMIGCDNEQCPIEWFHFSCVSLTYKHKGKWYCPKCRGDNEKTMDKSTEKTKK
 ROD 09-SEP-2000
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                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                    Direct Submission Submission Submitted (16-JUL-1998) Laboratory of Human Carcinogenesis, National Cancer Institute, National Institutes of Health, 37 Convent Dr., Bldg. 37, Rm. 2C01, Bethesda, MD 20892, USA Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 1001;
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mRNA linear complete cds.
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Nagashima,M., Hagiwara,K., Hancock,A.R. and
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Pred. No. 1.2e-153;
0; Mismatches 111;
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1001 bp
p33ING2 (Ing2) mRNA,
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/organism="Mus musculus"
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/product="p33ING2"
                                       AF078834.1 GI:10039542
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/gene="Ing2"
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il Similarity 88.1%;
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I (Dases I to 108424)

Muzny,D.W., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C., Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Ayele,M., Banks,T., Barbord,J., Benton,J., Bimage,K., Blankenburg,K., Bonnin,D., Buck,J., Burch,P., Burkett,C., Burrell,R.L., Byrd,N.C., Carron,T.F., Carter,M., Cavazos,S.R., Chacko,J. Chavez,D., Chen,G., Chen,Z., Chowdhry,I., Christopoulos,C., Carron,T.F., Carter,M., Cavazos,S.R., Chacko,J. Chavez,D., Chen,G., Cox,C., Coyle,M.D., Dathorne,S.R., David,R., David,R., Davis,C., Davy-Carroll,L., Dederich,D.A., David,R., Dalandy,K.R., Darger,H., Dugan-Rocha,S., Durbin,K.J., Barnhart,C., Edgar,D., Edwards,C.C., Elhaj,C., Escotto,M., Falls,T., Ferraguco,D., Flagy,N., Ford,J., Foster,P., Frantz,P., Gorrell,J.H., Guevara,W., Ganrer,T., Garza,N., Gill,R., Gorrell,J.H., Guevara,W., Gunaratne,P., Hale,S., Hamilton,K., Harris,C., Harris,K., Hart,M., Havlak,P., Hames,A., Hennandez,O., Howard,S., Holloway,C., Hollins,B., Jacksloson,B., Jia,Y., Johnson,R., Jolivet,S., Joudah,S., Kratson,E., Kally,S., Huber,J., Hulyk,S., Hume,J., Lewis,L., Li,J., Li,Z., Lichtarge,O., Lieu,C., Liu,J., Liu,W., Loulseged,H., Lozado,R.J., Lu,X., Lucier,A., Lucier,R., Lucier,R., Luna,R., Lucier,R., Lucier,R., Luna,R., Lucier,R., Lucier,R., Luna,R., Lucier,R., Luna,R., Lucier,R., Luna,R., Lucier,R., Luna,R., Lucier,R., Lucier,R., Luna,R., Lucier,R., Luci
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                                                AAGATCGAGGTAGTAAAAGGCCATCCACATTTTAAAAGGGTTATTTGTCTTTTATATATTC
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          Massey, E., Mawhiney, E., Matchin, F., Maatchindle, A., Matchine, E., Massey, E., Mawhiney, E., Mitchell, T., Mohabbat, K., Morgan, M., Metzker, M., Miner, G., Miner, Z., Mitchell, T., Mohabbat, K., Morgan, M., Morris, S., Mosten, M., Mowten, M., Nowchen, M., Nowchen, M., Nowchen, M., Owledo, R., Payton, B., Peerry, J., Perez, L., Oragunye, N., Oviedo, R., Pace, A., Payton, B., Peerry, J., Perez, L., Petres, L., Pickens, K., Primus, E., Pull. L., Quilles, M., Ren, Y., Rives, M., Rojas, A., Rojas, A., Rojas, A., Rojas, A., Rojas, M., Tabor, M., Stanley, H., Stone, H., Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, K., Tang, H., Tansey, J., Taylor, C., Taylor, T., Telfrod, B., Thomas, N., Thomas, S., Wang, S., Ward-Moore, S., Warren, R., Washington, C., Watlington, S., Williams, G., Williamson, A., Wleczyk, R., Wooden, S., Watlington, S., Weinstock, G. and Gibbs, R., Corrilla, S., Nelson, D., Weinstock, G., and Gibbs, R., Corrilla, S., Nelson, D., Williams, G., Milliamson, A., Milliams, G., Mil
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NOTE: This is a 'working draft' sequence. It currently consists of 50 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as'it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (19-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequencing vector: Plasmid;
Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly; program: Phrap; version 0.990329
Consensus quality: 115858 bases at least Q40
Consensus quality: 122576 bases at least Q30
Consensus quality: 127579 bases at least Q30
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Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
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5 157404: gap of unknown length
5 16845: contig of 10841 bp in length
Location/Qualifiers
                                                                                                        Score 686.8; DB 2;
Pred. No. 4.4e-137;
0; Mismatches 77;
                                          1. .168245
/organism="Rattus norvegicus"
/db_xref="taxon:10116"
/clone="6R330-12993"
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Best Local Similarity 90.5%;
Matches 744; Conservative
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                                                                                                         Euteleostomi;
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Direct Submitsion
Submitted (15-MAR-2002) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St.
                                                                                                                                                                                                                              Sequencing Center, Washington 4444 Forest Park Parkway, St.
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Center code: WUGSC
                                                                                                         Craniata; Vertebrata; E
Catarrhini; Hominidae;
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            Homo sapiens chromosome 4 clone R:
PROGRESS ***, 26 unordered pieces
42029 bp
e 4 clone 1
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Waterston, R.H.
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/note="assembly_name:Contig48"
2829. .3902
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20124. .21315
note-"assembly_name:Contig66"
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/note="assembly_name:Contig71"
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5163. :6294
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[509. .2728
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15993; .17523
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of 1193
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of 1632
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1 42029: contig of 3239
Location/Qualifiers
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                                                                 Score 574.6; DB 2;
Pred. No. 4.8e-113;
0; Mismatches 104;
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/note="assembly_name:Contig74"
32567 .34198
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34299 .36268
/note="assembly_name:Contig76"
36369 .38690
/note="assembly_name:Contig77"
38791 .42029
/note="assembly_name:Contig78"
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Best Local Similarity 84.7*
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                                                               Wagner, M.J., Gogela-Spehar, M., Skirrow, R.C., Johnston, R.N., Riabowol, K. and Helbing, C.C.
Expression of Novel ING Variants Is Regulated by Thyroid Hormone in
                                                                                                                                                                                                                                                                                                                                                                                                    /translation="MGQQQHLHYSPGSSAAEDSQLVSYVEEYLECVESLPLEIQRSV
TLLREIDSOGREALKEVDDVFEKHSNESDAHHKRILLQQLQRALIMTQELGDDKIQLV
TQVFEFIENRTKQMESLCKGFFDQEESDKSMEKSKVESNASRSTRRENRGNNSESHD
LCHWYNGMDDLEEQPPEKKEKSKKKRSSKKKRRSKAKQEREVSPIPFAIDPNEPTYCLCNQV
SFGEMIGCDNDECTIEWFHFSCVGLTYKPKGKWYCPDCRGDNEYTMNNTDKTKKDRR
                                                                                                                                                                                                     and Microbiology, University
Victoria, British Columbia V8W
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            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus.
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Helbing, C.C., Wagner, M.J., Gogela-Spehar, M., Skirrow, R.C.,
Johnston, R.N. and Rlabowol, K.
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                                                                                                      the Xenopus laevis Tadpole
J. Biol. Chem. 276 (50), 47013-47020 (2001)
11600495
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Pred. No. 7.4e-83;
0; Mismatches 312;
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Submitted (16-NOV-2000) Biochemistry
of Victoria, P.O. Box 3055 Stn. CSC,
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                                                                                                                                                                                                                                                                      /organism="Xenopus laevis"
/db_xref="taxon:8355"
                                                                                                                                                                                                                                                                                                                                   /note-"ING1-like protein"
                                                                                                                                                                                                                                                                                                                                                              /product="p32INGL"
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/db_xref="G1:17864715"
                                                                                                                                                                                                                                                                                                /tissue_type="brain"
/dev_stage="tadpole"
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ilarity 66.4%;
Conservative
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Wurny, D.M., Adams, C., Adio-Oduola, B., Ali-Osman, F.R., Allen, C., Adioroks, S.L., Amaratunge, H.C., Are, J.R., Ayele, M., Banks, T., Balbytooks, S.L., Amaratunge, H.C., Are, J.R., Ayele, M., Banks, T., Barbaria, J., Bewie, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Bungc, Y., Burch, P., Burkett, C., Burchl, K.L., Byrd, N.C., Carron, T.F., Carrer, M., Cavazcos, S.R., Chacko, J., Chavez, D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Dayy-Carroll, L., Dederich, D.A., David, R.J., Draper, H., Dugan-Rochas, S., Durbin, K.J., Dayer, C., C., Elhaj, C., Escotto, M., Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P., Garrell, J. H., Guevara, W., Ganner, T., Garza, N., Harls, K., Hart, M., Havlak, P., Hade, S., Hamilton, K., Harris, C., Howard, S., Huber, J., Hulle, S., Hume, J., Jackson, L. E., Jacobson, R., Howard, S., Huber, J., Hully, S., Hume, J., Jackson, L. E., Jacobson, R., Jia, Y., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C., AC129658 188087 bp DNA linear HTG 31-JUL-2002 Rattus norvegicus clone CH230-6112, *** SEQUENCING IN PROGRESS ***, 69 unordered pieces. 978 979 TAGGGTAAATGCATAAGACTATGCAATAATTTTTAATCATTAGTATTAATGGTGTATTAA 1038 992 TAAAGAAACTGTTTTAGATACAATGTGATATTTTAATAGTACTGAAATATTAAAACCTTT 1051 678 918 653 713 738 833 828 893 953 GATGATAGGATGTGACAATGAACAGTGTCCAATTGAATGGTTTCACTTTTCATGTTTC 798 Euteleostomi; 534 ATCTGAAAGGTCTACACGTAGGCCTCGCAGACAGCGCAATAGTGAGAGCCACGACTTGTG 919 ATCCACATITTAAAGGGTTATTTGTCTTTTATAATTCGTTTGCTTTCAGAAAATGTTT TCACATGGCAAATGGGATTGAAGACTGTGATGATCAGCCACCTAAAGAAAAGAAATCCAA GTCAGCAAAGAAAAGAAACGCTCCAAGGCCAAGCAGAAAGGGAAAGCTTCACCTGTTGA GTTTGCAATAGATCCTAATGAACCTACATACTGCTTATGCAACCAAGTGTCTTATGGGGA ACTTACCTACAAACCAAAGGGCAAATGGTATTGTCCTGACTGCAGAGGACAATGAAAA ACTTACCTATAAACCAAAGGGGAAATGGTATTGCCCAAAGTGCAGGGGAGATAATGAGAA 859 AACAATGGACAAAAGTACTGAAAAGACAAAAAAGGATAGAAGATCGAGGTAGTAAAGGCC Norway rat. Rattus norvegicus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleost Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;

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Li,J., Lin, Kureshi,A., Landry,N., Leal,B., Lewis,L.C., Lewis,L.,
Li,J., Li,Z., Luchtange,O., Lieu,C., Liu,W., Lulu,W., Loulseged,H.,
Lozado,R.J. Lu,X., Lucier,A., Lucier,R., Mar,J.,
Maheshwari,M., Maplua,P., Martin,R., Martindale,A., Martinez,E.,
Massey,E., Mawhiney,E., McLeod,M.P., Meador,M., Mel,G., Metzker,M.,
Miner,G., Miner,Z., Mitchell,T., Mohabbat,K., Morgan,M., Mortis,S.,
Moser,M., Neal,D., Newtson,J., Newtson,N., Nguyen,A., Nguyen,N.,
Nguyen,N., Nickerson,E., Nwokenkwo,S., Oguh,M., Okwuou,G.,
Peters,L., Pickenson,E., Pace,A., Payton,B., Peery,J., Perez,L.,
Peters,L., Pickenson,E., Nwokenkwo,S., Oguh,M., Okwuou,G.,
Rives,M., Rojas,A., Rojubokan,I., Rolfe,M., Ruiz,S., Savery,G.,
Scherer,S., Scott,G., Shen,H., Shooshtari,N., Sisson,I.,
Sutton,A., Svatek,A., Tabor,P., Tamerias,A., Tameriss,K., Tansey,J., Taylor,C., Taylor,T., Talfrod,B., Thomas,N., Thomas,S.,
Usmani,K., Ward-Moore,S., Warren,R., Washington,C., Watlington,S.,
Walliams,G., Williamson,A., Waleczyk,R., Wooden,S., Worley,K.,
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NOTE: This is a 'working draft' sequence. It currently consists of 69 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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/translation="Mispangeoihlunivedyldsieslppdlgrnyslmreidaky
QEILKELDDYYEKFRETDGTQKRRYLHCIORALIBSQELGDEKIOIVSQWYELVERR
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SYGEMIGCDNDECPIEWFHFSCVGLNHKPKGKWYCPKCRGESEKTMDKALEKSKKERA
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0; Mismatches 287;
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                                                                             /product="p33ING1 protein"
/protein_id="AAF09183.1"
/db_xref="G1:6456562"
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                            /organism="Mus musculus'
                                        /db_xref="taxon:10090
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
1 (bases 1 to 840)
Rancourt, D. and Garkavtsev, I.
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Submitted (11-MAY-1999) Genome Therapeutics Corp., 100
Waltham, MA 02453, USA
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Zeremski,M., Hill,J.E., Kwek,S.S., Grigorian,I.A., Gurova,K.V., Garkavtsev,I.V., Diatchenko,L., Koonin,E.V. and Gudkov,A.V. Structure and regulation of the mouse ingl gene. Three alternative
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116 ACCGGGGAGCGGAGCCGGCTGCTCACCTGCTGCAGGACTACCTTGAGTGCGTGGAG 175
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="Mammary tumor. WAP-TGF alpha model. 7 months old, gross tissue." /clone_lib="NCI_CGAP_Mam5" /lab_host="DH108"
                                                                                                                                           BC016573 Honditor of growth family, member 1, clone MGC:27881 IMAGE:349601;3, mRNA, complete cds.
                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 1584)
                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
Submitted (31-CCT-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            X., Hulyk, S.W., Hale, S.M.,
S., Martin, R.G., Muzny, D.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapb2-remail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing Center
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Pred. No. 3.1e-44;
0; Mismatches 289; Indels 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amgebcm.tmc.edu
Gunaratne, P.H., Garcla, A.M., Lu, X., Huly
Yoon, V.S., Kowis, C.R., Lawrence, S., Mart
Richards, S., Gibbs, R.A.
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                            897
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389 .1228
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TITLE
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Direct Submission
Submitted (16-1999) Molecular Genetics, Univ. of Illinois at
Chicago, 900 South Ashland Ave., Chicago, IL 60607, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGCAGCGGCAAGGCGGGCCAGGACAAGTCGAAGAGTGAGGCCATCACACAGGCAGATAAG
transcripts encode two phd finger proteins that have opposite effects on p53 function J. Biol. Chem. 274 (45), 32172-32181 (1999)
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CAGGTGGACAGTGAGGGCTCTTGGAAGCACACCAGGACATCAGTGACGGCACTGGT
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Pred. No. 3.5e-44;
0; Mismatches 289;

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